

OM protein - protein search, using sw model  
 Run on: May 12, 2006, 21:13:34 ; Search time 185 Seconds  
 (without alignments)  
 211.377 Million cell updates/sec

Title: US-10-063-557-50  
 Perfect score: 461  
 Sequence: 1 MERVTLALLLLAGLTALLEAN.....HSPVPEKAIPITPGSATTC 89  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5  
 2443163 seqs, 439378781 residues  
 Total number of hits satisfying chosen parameters: 2443163  
 Minimum DB seq length: 0  
 Maximum DB seq length: 200000000  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 1500 summaries

Database :  
 1: Geneseq\_21.\*  
 2: Geneseqp1980s.\*  
 3: Geneseqp1990s.\*  
 4: Geneseqp2000s.\*  
 5: Geneseqp2001s.\*  
 6: Geneseqp2002s.\*  
 7: Geneseqp2003as.\*  
 8: Geneseqp2003bs.\*  
 9: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	DB ID	Description
RESULT 1				
ID	AA56705	standard; protein; 89 AA.		
DE	Membrane-bound protein PRO1069.			
PN	WO9963088-A2.			
PD	09-DEC-1999.			
PA	(GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 461;	DB 3;	Length 89;
Best Local Similarity	100.0%;	Pred. No. 4e-50;		
RESULT 2				
ID	AA57258	standard; protein; 89 AA.		
DE	Human signal peptide containing protein HSP35 SEQ ID NO:35.			
PN	WO20000610-A2.			
PD	06-JAN-2000.			
PA	(INCY-) INCYTE PHARM INC.			
Query Match	100.0%;	Score 461;	DB 3;	Length 89;
Best Local Similarity	100.0%;	Pred. No. 4e-50;		
RESULT 3				
ID	AA5679	standard; protein; 89 AA.		
DE	Human kidney disease associated protein SEQ ID 11.			
PN	WO200061622-A2.			
PD	19-OCT-2000.			
PA	(INCY-) INCYTE PHARM INC.			
Query Match	100.0%;	Score 461;	DB 3;	Length 89;
Best Local Similarity	100.0%;	Pred. No. 4e-50;		
RESULT 4				
ID	AA29123	standard; protein; 89 AA.		
DE	Human PRO polypeptide sequence #100.			
PN	WO200168848-A2.			
PD	20-SEP-2001.			
PA	(GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 461;	DB 4;	Length 89;
Best Local Similarity	100.0%;	Pred. No. 4e-50;		
RESULT 5				
ID	AA87550	standard; protein; 89 AA.		
DE	Human PRO1069.			
PN	WO200116318-A2.			
PD	08-MAR-2001.			
PA	(GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 461;	DB 4;	Length 89;
Best Local Similarity	100.0%;	Pred. No. 4e-50;		
RESULT 6				
ID	AA65228	standard; protein; 89 AA.		
DE	Human PRO1069 (UNQ526) protein sequence SEQ ID NO:262.			

PN WO200073454-A1.  
 PD 07-DEC-2000.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 461; DB 4; Length 89;  
 Best Local Similarity 100.0%; Pred. No. 4e-50;  
 RESULT 7  
 ID ABG95875 standard; protein; 89 AA.  
 DE Human secreted/transmembrane protein PRO1069.  
 PN US2002119130-A1.  
 PD 29-AUG-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 461; DB 5; Length 89;  
 Best Local Similarity 100.0%; Pred. No. 4e-50;  
 RESULT 8  
 ID ABUS8499 standard; protein; 89 AA.  
 DE Human PRO polypeptide #100.  
 PN US2003027272-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 461; DB 6; Length 89;  
 Best Local Similarity 100.0%; Pred. No. 4e-50;  
 RESULT 9  
 ID ABUS8047 standard; protein; 89 AA.  
 DE Novel human secreted and transmembrane protein PRO1069.  
 PN US2003032127-A1.  
 PD 13-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 461; DB 6; Length 89;  
 Best Local Similarity 100.0%; Pred. No. 4e-50;  
 RESULT 10  
 ID ABUS84362 standard; protein; 89 AA.  
 DE Human secreted/transmembrane protein (PRO) #100.  
 PN US2003032112-A1.  
 PD 13-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 461; DB 6; Length 89;  
 Best Local Similarity 100.0%; Pred. No. 4e-50;  
 RESULT 11  
 ID ABR66236 standard; protein; 89 AA.  
 DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
 PN US2003027278-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 461; DB 6; Length 89;  
 Best Local Similarity 100.0%; Pred. No. 4e-50;  
 RESULT 12  
 ID ABR65626 standard; protein; 89 AA.  
 DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
 PN US2003036159-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 461; DB 6; Length 89;  
 Best Local Similarity 100.0%; Pred. No. 4e-50;  
 RESULT 13  
 ID ABUS9566 standard; protein; 89 AA.  
 DE Human secreted/transmembrane protein (PRO) #100.  
 PN US2003040070-A1.  
 PD 27-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 461; DB 6; Length 89;  
 Best Local Similarity 100.0%; Pred. No. 4e-50;  
 RESULT 14  
 ID ABUS8043 standard; protein; 89 AA.  
 DE Human PRO polypeptide #75.  
 PN US2003027163-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 461; DB 6; Length 89;  
 Best Local Similarity 100.0%; Pred. No. 4e-50;  
 RESULT 15  
 ID ABUS9121 standard; protein; 89 AA.  
 DE Novel human secreted or transmembrane protein PRO1069.  
 PN US2002132252-A1.  
 PD 19-SEP-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 461; DB 6; Length 89;  
 Best Local Similarity 100.0%; Pred. No. 4e-50;  
 RESULT 16  
 ID ABUS2633 standard; protein; 89 AA.  
 DE Human secreted/transmembrane protein PRO1069.

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PN US2003032023-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 17
ID ABU82805 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 18
ID ABU89926 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 19
ID ABR68175 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 20
ID ABU60552 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, #105.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 21
ID ABU96228 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 22
ID ABU92659 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 23
ID ABO08736 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 24
ID ABO02788 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 25
ID ABR74942 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 26
ID ABR94704 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 27
ID ABU13934 standard; protein; 89 AA.
DE Human PRO1069 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH ) GENENTECH LTD.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 28
ID ABU85677 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 29
ID ABU98837 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 30
ID ABU98052 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 31
ID ABU91758 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 32
ID ABU89451 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 33
ID ABU86292 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 34
ID ABU67505 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 35
ID ABU80533 standard; protein; 89 AA.
DE Human PRO protein #100.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 36
ID ABU72519 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
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ID ASU85062 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 47  
ID ABO0201 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 48  
ID ABO11533 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 49  
ID ABO02178 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 50  
ID ASU88752 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 51  
ID ASU83447 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 52  
ID ABO06248 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 53  
ID ABR59284 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 54  
ID ABO09346 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 55  
ID ABO19210 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 56  
ID ABO11228 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.

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PN US2003036123-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 57
ID ABR66846 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 58
ID ABO16059 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 59
ID ABO13765 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 60
ID ABU71530 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 61
ID ABU65668 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, SEQ ID 200.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 62
ID ABO07516 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 63
ID ABO03703 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 64
ID ABR67151 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 65
ID ABO15754 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 66
ID ABU56035 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, PRO1069.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 67
ID ABU72311 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 68
ID ABU65363 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 69
ID ABU95308 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 70
ID ABU71211 standard; protein; 89 AA.
DE Human PRO1069 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 71
ID ABO07821 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 72
ID ABR70062 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 73
ID ABR69395 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 74
ID ABO01536 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003008353-A1.
PD 03-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 75
ID ABU81338 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 76
ID ABR60135 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032137-A1.
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PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 77
ID ABU90984 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 78
ID ABR67870 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 79
ID ABR65258 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 80
ID ABR68480 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 81
ID ABR71892 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 82
ID ABUS9268 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, #105.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 83
ID ABUS3372 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 84
ID ABUS9062 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 85
ID ABUS3142 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 86
ID ABUS4998 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 87
ID ABUS90546 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 88
ID ABUS4057 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 89
ID ABUS3708 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 90
ID ABO25965 standard; protein; 89 AA.
DE Human PRO1069 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 91
ID ABR64953 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 92
ID ABO27305 standard; protein; 89 AA.
DE Human secreted/transmembrane polypeptide PRO1069.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 93
ID ABR68785 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 94
ID ABO06601 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 95
ID ABR99146 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 96
ID ABUS7030 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003027280-A1.
PD 06-FEB-2003.
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Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 97
ID ABU82269 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 98
ID ABU82269 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 99
ID ABU82280 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 100
ID ABU83752 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 101
ID ABO08126 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 102
ID ABU92500 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 103
ID ABU81837 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 104
ID ABU66001 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 105
ID ABU81170 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 106
ID ABR59830 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 107
ID ABU94018 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 108
ID ABU99871 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 109
ID ABR66541 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 110
ID ABR90959 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 111
ID BAO53285 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 112
ID ABU58974 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, #105.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 113
ID ABU94386 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 114
ID ABU79268 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032186-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 115
ID ABU86597 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 116
ID ABU86902 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
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Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 117
ID ABU94691 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 118
ID ABO04618 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 119
ID ABR70367 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 120
ID ABU92352 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 121
ID ABU98532 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 122
ID ABR65931 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 123
ID ABR64648 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 124
ID ABU59417 standard; protein; 89 AA.
DE Novel human secreted or transmembrane protein PRO1129.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 125
ID ABU79573 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 126
ID ABU92964 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 127
ID ABU84667 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 128
ID ABU91143 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 129
ID ABU90236 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 130
ID ABO09651 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 131
ID ABO10923 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 132
ID ABR70977 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 133
ID ABU98287 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 134
ID ABU87585 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 135
ID ABU91453 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 136
ID ABU92922 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 137
ID ABU84667 standard; protein; 89 AA.
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DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 138
ID ABR69757 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 139
ID ABU80134 standard; protein; 89 AA.
DE Human PRO protein #100.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 140
ID ABU82499 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 141
ID ABU92183 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 142
ID ABU93403 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 143
ID ABO09956 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 144
ID ABO09041 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 145
ID ABU96463 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 146
ID ABU10889 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 147
ID ABU10609 standard; protein; 89 AA.
DE Human secreted/transmembrane protein #100.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 148
ID ABU81641 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 149
ID ABU72133 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 150
ID ABU95618 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 151
ID ABU96827 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 152
ID ABR70672 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 153
ID ABO05023 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 154
ID ABO08431 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 155
ID ABU88580 standard; protein; 89 AA.
DE Human secreted and transmembrane polypeptide PRO1069.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 156
ID ABO34094 standard; protein; 89 AA.
DE Human PRO1069 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
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Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 157  
ID ABO05638 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 158  
ID ABR74027 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 159  
ID ABR95619 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 160  
ID ABR80916 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 161  
ID ABR81221 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 162  
ID ABR00917 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 163  
ID ABR88519 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 164  
ID ABR77340 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 165  
ID ABO28024 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 166  
ID ABO31569 standard; protein; 89 AA.

DE Human secreted/transmembrane protein (PRO) #100.  
FN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
Pred. No. 4e-50;  
RESULT 167  
ID ABM07986 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
FN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
Pred. No. 4e-50;  
RESULT 168  
ID AB040466 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
FN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
Pred. No. 4e-50;  
RESULT 169  
ID AB035891 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
FN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
Pred. No. 4e-50;  
RESULT 170  
ID AB044030 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
FN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
Pred. No. 4e-50;  
RESULT 171  
ID ADA77952 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
FN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
Pred. No. 4e-50;  
RESULT 172  
ID ABM44825 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
FN US2003104539-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
Pred. No. 4e-50;  
RESULT 173  
ID AB003093 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
FN US2003036131-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
Pred. No. 4e-50;  
RESULT 174  
ID ABR30349 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
FN US2003040075-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
Pred. No. 4e-50;  
RESULT 175  
ID ABM17263 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
FN US2003054459-A1.  
PD 20-NAR-2003.  
PA (GETH ) GENENTECH INC.

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Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 176
ID ABR95009 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US200304930-A1.
PD 06-MAR-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 177
ID ABR95314 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 178
ID ADB17107 standard; protein; 89 AA.
DE Human transmembrane PRO polypeptide (SeqID 50).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 179
ID ABO21552 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 180
ID ABR97816 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 181
ID ABR87604 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 182
ID ABM77645 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 183
ID ABM27875 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 184
ID ABM06156 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 185
ID ABM16043 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 186
ID ABM35113 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 187
ID ABM26350 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 188
ID ABO48132 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 189
ID ABR92874 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003084462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 190
ID ABO24635 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 191
ID ADA37773 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 192
ID ABM11646 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003084447-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 193
ID ABM02747 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 194
ID ABM16043 standard; protein; 89 AA.
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DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
RESULT 195  
ID ABO27604 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
RESULT 196  
ID ABO29095 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
RESULT 197  
ID ABO07071 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
RESULT 198  
ID ABO21165 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
RESULT 199  
ID ABO09511 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
RESULT 200  
ID ABO41381 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
RESULT 201  
ID ABO36196 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
RESULT 202  
ID ABO43725 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
RESULT 203  
ID ABO76425 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
RESULT 204  
ID ABO76121 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
RESULT 205  
ID ABO25740 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
RESULT 206  
ID ABO26045 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
RESULT 207  
ID ABO21459 standard; protein; 89 AA.  
DE Human secreted/transmembrane polypeptide PRO1069.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
RESULT 208  
ID ABO03398 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
RESULT 209  
ID ABO02483 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
RESULT 210  
ID ABO44263 standard; protein; 89 AA.  
DE Human secreted/transmembrane polypeptide PRO 1069.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
RESULT 211  
ID ABO90654 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
RESULT 212  
ID ABO73722 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;  
RESULT 213  
ID ABO16974 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.

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PN	US2003068733-A1.				
FD	10-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					
Best Local Similarity	100.0%;	Score 461;	DB 6;	Length 89;	
RESULT 242					
ID	ABM15306 standard; protein; 89 AA.				
DE	Human secreted polypeptide PRO1069, SEQ ID NO:200.				
FN	US2003068692-A1.				
PD	10-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					
Best Local Similarity	100.0%;	Score 461;	DB 6;	Length 89;	
RESULT 243					
ID	ABM06461 standard; protein; 89 AA.				
DE	Human secreted polypeptide PRO1069, SEQ ID NO:200.				
FN	US2003068709-A1.				
PD	10-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					
Best Local Similarity	100.0%;	Score 461;	DB 6;	Length 89;	
RESULT 244					
ID	ABM04272 standard; protein; 89 AA.				
DE	Human secreted polypeptide PRO1069, SEQ ID NO:200.				
FN	US2003068716-A1.				
PD	10-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					
Best Local Similarity	100.0%;	Score 461;	DB 6;	Length 89;	
RESULT 245					
ID	ABM22385 standard; protein; 89 AA.				
DE	Human secreted polypeptide PRO1069, SEQ ID NO:200.				
FN	US2003068740-A1.				
PD	10-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					
Best Local Similarity	100.0%;	Score 461;	DB 6;	Length 89;	
RESULT 246					
ID	ABM07681 standard; protein; 89 AA.				
DE	Human secreted polypeptide PRO1069, SEQ ID NO:200.				
FN	US2003068751-A1.				
PD	10-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					
Best Local Similarity	100.0%;	Score 461;	DB 6;	Length 89;	
RESULT 247					
ID	ABO40771 standard; protein; 89 AA.				
DE	Human secreted/transmembrane protein (PRO) #100.				
FN	US2003068684-A1.				
PD	10-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					
Best Local Similarity	100.0%;	Score 461;	DB 6;	Length 89;	
RESULT 248					
ID	ABM35418 standard; protein; 89 AA.				
DE	Human secreted polypeptide PRO1069, SEQ ID NO:200.				
FN	US2003073179-A1.				
PD	17-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					
Best Local Similarity	100.0%;	Score 461;	DB 6;	Length 89;	
RESULT 249					
ID	ABM33181 standard; protein; 89 AA.				
DE	Human secreted polypeptide PRO1069, SEQ ID NO:200.				
FN	US2003087374-A1.				
PD	08-MAY-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					
Best Local Similarity	100.0%;	Score 461;	DB 6;	Length 89;	
RESULT 250					
ID	ABO52707 standard; protein; 89 AA.				
DE	Human PRO polypeptide #100.				
FN	US2003049773-A1.				
PD	13-MAR-2003.				
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PN	US2003068733-A1.				
FD	10-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					
Best Local Similarity	100.0%;	Score 461;	DB 6;	Length 89;	
RESULT 242					
ID	ABM15306 standard; protein; 89 AA.				
DE	Human secreted polypeptide PRO1069, SEQ ID NO:200.				
FN	US2003068692-A1.				
PD	10-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					
Best Local Similarity	100.0%;	Score 461;	DB 6;	Length 89;	
RESULT 243					
ID	ABM06461 standard; protein; 89 AA.				
DE	Human secreted polypeptide PRO1069, SEQ ID NO:200.				
FN	US2003068709-A1.				
PD	10-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					
Best Local Similarity	100.0%;	Score 46			

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PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 251  
ID ABO50267 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 252  
ID ABU99261 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 253  
ID ABO04313 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 254  
ID ABO05943 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 255  
ID ABM18483 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 256  
ID ADA27898 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein PRO1069.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 257  
ID ABR97511 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 258  
ID ABR80611 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 259  
ID ABO01222 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 260  
ID ABR88824 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003096353-A1.  
PD 22-MAY-2003.

DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 261  
ID ABM13476 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 262  
ID ABM20860 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 263  
ID ABO41991 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 264  
ID ABO42601 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 265  
ID ABM10121 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 266  
ID ABO38636 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 267  
ID ABM32876 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 268  
ID ABM22690 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 269  
ID ABM74901 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003096353-A1.  
PD 22-MAY-2003.

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Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 270
ID ADA79744 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 271
ID ABR96291 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 272
ID ABR02442 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 273
ID ABR86384 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 274
ID ABR86689 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 275
ID ABR16653 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 276
ID ABR29705 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 277
ID ABO29129 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 278
ID ABR23910 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 279
ID ABO20332 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032125-A1.
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ID ABR23300 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 280
ID ABR22080 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 281
ID ABO37721 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 282
ID ABR28485 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 283
ID ABR28790 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 284
ID ABR66434 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 285
ID ABR75816 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 286
ID ABR34096 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 287
ID ABR34401 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 288
ID ABO20332 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032125-A1.
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PD 13-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 289  
ID ABO21247 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 290  
ID ABO22162 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 291  
ID ADA20084 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 292  
ID ABO34191 standard; protein; 89 AA.  
DE Human secreted/transmembrane polypeptide PRO 1069.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 293  
ID ABR96596 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 294  
ID ADA94478 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein PRO1069.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 295  
ID ABR85774 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 296  
ID ABR99756 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 297  
ID ABM00612 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 298

ID ABM00307 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 299  
ID ABO29739 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003088700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 300  
ID ABM23605 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 301  
ID ABM29400 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 302  
ID ABO38331 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003088767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 303  
ID ABO45631 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 304  
ID ABM20555 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 305  
ID ADA81471 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003052121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 306  
ID ABO16669 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003027276-A1.  
PD 05-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 307  
ID ABO18295 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003044920-A1.

PD 06-MAR-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 308  
ID ABO22722 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 309  
ID ABO23027 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 310  
ID ABR92569 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 311  
ID ABR81526 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 312  
ID ABM77950 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 313  
ID ABR89739 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003073171-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 314  
ID ABM26655 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 315  
ID ABM13781 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 316  
ID ABO28519 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 317  
ID ABO48437 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.

ID ABO30349 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 318  
ID ABM07376 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 319  
ID ABM03967 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 320  
ID ABO37111 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 321  
ID ABO41686 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 322  
ID ABO35281 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 323  
ID ABM25130 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 324  
ID ABO47522 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 325  
ID ABO47827 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 326  
ID ABO48437 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.

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PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 327
ID ABO51487 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 328
ID ABO51792 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 329
ID ABO50572 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 330
ID ABR79696 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 331
ID ABM16958 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 332
ID ABO17990 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 333
ID ABO20942 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 334
ID ABR96901 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 335
ID ADA38703 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 336
ID ABM12256 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 337
ID ABM16348 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 338
ID AEM24215 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 339
ID ABM14696 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003058696-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 340
ID ABM04577 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 341
ID ABM06766 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 342
ID ABM09206 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 343
ID ABO39246 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003088775-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 344
ID ABM75511 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 345
ID ABM25435 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
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DE US2003104541-A1.
PN 05-JUN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 346
ID ABM19945 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 347
ID ABO46851 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 348
ID ABO47156 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 349
ID ADA83269 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 350
ID ABR71587 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 351
ID ABR72197 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 352
ID ABR98536 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 353
ID ABO06906 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 354
ID ABR84859 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 355
ID ABR73417 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 356
ID ABR76511 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 357
ID ABR73112 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 358
ID ABR18178 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 359
ID ABO20637 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 360
ID ABO25380 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 361
ID ABO25685 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 362
ID ABR94094 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 363
ID ADA92824 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 364
ID ABR80001 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
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RESULT 365
ID ABO11341 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
Pred. No. 4e-50;
RESULT 366
ID ABO32948 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
Pred. No. 4e-50;
RESULT 367
ID ABO30654 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
Pred. No. 4e-50;
RESULT 368
ID ABO30959 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
Pred. No. 4e-50;
RESULT 369
ID ABM27265 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
Pred. No. 4e-50;
RESULT 370
ID ABM30010 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
Pred. No. 4e-50;
RESULT 371
ID ABM05546 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
Pred. No. 4e-50;
RESULT 372
ID ABM15611 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
Pred. No. 4e-50;
RESULT 373
ID ABM08596 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
Pred. No. 4e-50;
RESULT 374
ID ABO42296 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
Pred. No. 4e-50;
RESULT 375
ID ABO38026 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
Pred. No. 4e-50;
RESULT 376
ID ABO45936 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
Pred. No. 4e-50;
RESULT 377
ID ABM66739 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
Pred. No. 4e-50;
RESULT 378
ID ADB20312 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
Pred. No. 4e-50;
RESULT 379
ID ABM19640 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
Pred. No. 4e-50;
RESULT 380
ID ABO49352 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
Pred. No. 4e-50;
RESULT 381
ID ABO49657 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
Pred. No. 4e-50;
RESULT 382
ID ADA78564 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
Pred. No. 4e-50;
RESULT 383
ID ABR88214 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
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PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 384
ID ADA00381 standard; protein; 89 AA.
DE Human secreted/transmembrane polypeptide PRO 1069.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 385
ID ABM26960 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 386
ID ABM03357 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 387
ID ABO39856 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 388
ID ABO49962 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 389
ID ABO50877 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 390
ID ABO05333 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 391
ID ABR74637 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 392
ID ABR77116 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 393
ID ABM17873 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 394
ID ABR95924 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 395
ID ABO21857 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 396
ID ABO20027 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 397
ID ABO24330 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 398
ID ABR86079 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 399
ID ABM10731 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 400
ID ABM76730 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 401
ID ABR89434 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 402
ID ABM12561 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
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ID	17-APR-2003.						
PA	(GETH ) GENENTECH INC.						
Query Match							
Best Local Similarity	100.0%; Score 461; DB 7; Length 89;						
Predicted No.	4e-50;						
<b>RESULT 403</b>							
ID	ABM05851 standard; protein; 89 AA.						
DE	Human secreted polypeptide PRO1069, SEQ ID NO:200.						
PN	US2003068717-A1.						
PD	10-APR-2003.						
PA	(GETH ) GENENTECH INC.						
Query Match							
Best Local Similarity	100.0%; Score 461; DB 7; Length 89;						
Predicted No.	4e-50;						
<b>RESULT 404</b>							
ID	ABO34976 standard; protein; 89 AA.						
DE	Human PRO polypeptide #100.						
PN	US2003068728-A1.						
PD	10-APR-2003.						
PA	(GETH ) GENENTECH INC.						
Query Match							
Best Local Similarity	100.0%; Score 461; DB 7; Length 89;						
Predicted No.	4e-50;						
<b>RESULT 405</b>							
ID	ABM03052 standard; protein; 89 AA.						
DE	Human secreted polypeptide PRO1069, SEQ ID NO:200.						
PN	US2003068764-A1.						
PD	10-APR-2003.						
PA	(GETH ) GENENTECH INC.						
Query Match							
Best Local Similarity	100.0%; Score 461; DB 7; Length 89;						
Predicted No.	4e-50;						
<b>RESULT 406</b>							
ID	ABM19030 standard; protein; 89 AA.						
DE	Human secreted polypeptide PRO1069, SEQ ID NO:200.						
PN	US2003104550-A1.						
PD	05-JUN-2003.						
PA	(GETH ) GENENTECH INC.						
Query Match							
Best Local Similarity	100.0%; Score 461; DB 7; Length 89;						
Predicted No.	4e-50;						
<b>RESULT 407</b>							
ID	ABM19335 standard; protein; 89 AA.						
DE	Human secreted polypeptide PRO1069, SEQ ID NO:200.						
PN	US2003104551-A1.						
PD	05-JUN-2003.						
PA	(GETH ) GENENTECH INC.						
Query Match							
Best Local Similarity	100.0%; Score 461; DB 7; Length 89;						
Predicted No.	4e-50;						
<b>RESULT 408</b>							
ID	ABO46546 standard; protein; 89 AA.						
DE	Human PRO polypeptide #100.						
PN	US2003049761-A1.						
PD	13-MAR-2003.						
PA	(GETH ) GENENTECH INC.						
Query Match							
Best Local Similarity	100.0%; Score 461; DB 7; Length 89;						
Predicted No.	4e-50;						
<b>RESULT 409</b>							
ID	ABO49047 standard; protein; 89 AA.						
DE	Human secreted/transmembrane protein (PRO) #100.						
PN	US2003049757-A1.						
PD	13-MAR-2003.						
PA	(GETH ) GENENTECH INC.						
Query Match							
Best Local Similarity	100.0%; Score 461; DB 7; Length 89;						
Predicted No.	4e-50;						
<b>RESULT 410</b>							
ID	ABR69090 standard; protein; 89 AA.						
DE	Human secreted polypeptide PRO1069, SEQ ID NO:200.						
PN	US2003027273-A1.						
PD	06-FEB-2003.						
PA	(GETH ) GENENTECH INC.						
Query Match							
Best Local Similarity	100.0%; Score 461; DB 7; Length 89;						
Predicted No.	4e-50;						
<b>RESULT 411</b>							
ID	ABR89129 standard; protein; 89 AA.						
DE	Human secreted polypeptide PRO1069, SEQ ID NO:200.						
PN	US2003036119-A1.						
PD	20-FEB-2003.						
PA	(GETH ) GENENTECH INC.						
Query Match							
Best Local Similarity	100.0%; Score 461; DB 7; Length 89;						

[illegible]

Query Match	Best Local Similarity	Score	DB	Length
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.	US2003064444-A1.	100.0%;	DB 7;	Length 89;
PN US2003064444-A1.		100.0%;	Pred. No. 4e-50;	
PD 03-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 461;	DB 7;	Length 89;
Best Local Similarity	100.0%;	Pred. No. 4e-50;		
RESULT 422				
ID ABO29434 standard; protein; 89 AA.				
DE Human secreted/transmembrane protein (PRO) #100.				
PN US2003068697-A1.				
PD 10-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 461;	DB 7;	Length 89;
Best Local Similarity	100.0%;	Pred. No. 4e-50;		
RESULT 423				
ID ABO31264 standard; protein; 89 AA.				
DE Human secreted/transmembrane protein (PRO) #100.				
PN US2003068710-A1.				
PD 10-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 461;	DB 7;	Length 89;
Best Local Similarity	100.0%;	Pred. No. 4e-50;		
RESULT 424				
ID ABM4391 standard; protein; 89 AA.				
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.				
PN US2003068686-A1.				
PD 10-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 461;	DB 7;	Length 89;
Best Local Similarity	100.0%;	Pred. No. 4e-50;		
RESULT 425				
ID ABM09816 standard; protein; 89 AA.				
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.				
PN US2003073178-A1.				
PD 17-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 461;	DB 7;	Length 89;
Best Local Similarity	100.0%;	Pred. No. 4e-50;		
RESULT 426				
ID ABO38941 standard; protein; 89 AA.				
DE Human secreted/transmembrane protein (PRO) #100.				
PN US2003068774-A1.				
PD 10-APR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 461;	DB 7;	Length 89;
Best Local Similarity	100.0%;	Pred. No. 4e-50;		
RESULT 427				
ID ABM34706 standard; protein; 89 AA.				
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.				
PN US2003104538-A1.				
PD 05-JUN-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 461;	DB 7;	Length 89;
Best Local Similarity	100.0%;	Pred. No. 4e-50;		
RESULT 428				
ID ABO51182 standard; protein; 89 AA.				
DE Human secreted/transmembrane protein (PRO) #100.				
PN US2003049781-A1.				
PD 13-MAR-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 461;	DB 7;	Length 89;
Best Local Similarity	100.0%;	Pred. No. 4e-50;		
RESULT 429				
ID ABO04008 standard; protein; 89 AA.				
DE Human secreted/transmembrane protein (PRO) #100.				
PN US2003036158-A1.				
PD 20-FEB-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 461;	DB 7;	Length 89;
Best Local Similarity	100.0%;	Pred. No. 4e-50;		
RESULT 430				
ID ABO10478 standard; protein; 89 AA.				
DE Human PRO polypeptide #100.				
PN US2003036151-A1.				
PD 20-FEB-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 461;	DB 7;	Length 89;
Best Local Similarity	100.0%;	Pred. No. 4e-50;		
RESULT 431				
ID ABO53180 standard; protein; 89 AA.				
DE Human secreted/transmembrane protein PRO1069.				
PN US2003044806-A1.				
PD 06-MAR-2003.				
PA (GETH ) GENENTECH INC.				

PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 441  
ID ABO13171 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 442  
ID ABO31874 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 443  
ID ABO14086 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068683-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 444  
ID ABO40161 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 445  
ID ABO40161 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003068681-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 446  
ID ABO4596 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 447  
ID ABO33791 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 448  
ID ABO20250 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 449  
ID ABO48742 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 450  
ID ABO22550 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein PRO1069.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 451  
ID ABO72807 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 452  
ID ABO15449 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 453  
ID ABR83164 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 454  
ID ABO15144 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 455  
ID ABO17279 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 456  
ID ABO17568 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 457  
ID ADA06551 standard; protein; 89 AA.  
DE Human secreted/transmembrane PRO polypeptide #75.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 458  
ID ADA39244 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein PRO1069.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 459  
ID ABR85469 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;

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Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 460
ID ABO37416 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003088726-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
Pred. No. 4e-50;
RESULT 470
ID ABO75206 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
Pred. No. 4e-50;
RESULT 471
ID ABO33486 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
Pred. No. 4e-50;
RESULT 472
ID ABO46241 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
Pred. No. 4e-50;
RESULT 473
ID ADA82635 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
Pred. No. 4e-50;
RESULT 474
ID ADB85623 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
Pred. No. 4e-50;
RESULT 475
ID ADB96270 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
Pred. No. 4e-50;
RESULT 476
ID ABO31840 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
Pred. No. 4e-50;
RESULT 477
ID ABO31230 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
Pred. No. 4e-50;
RESULT 478
ID ADB85943 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
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Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 460
ID ABO77035 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
Pred. No. 4e-50;
RESULT 461
ID ABO28214 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
Pred. No. 4e-50;
RESULT 462
ID ABO22995 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
Pred. No. 4e-50;
RESULT 463
ID ABO30315 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
Pred. No. 4e-50;
RESULT 464
ID ABO21775 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
Pred. No. 4e-50;
RESULT 465
ID ABO21470 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
Pred. No. 4e-50;
RESULT 466
ID ABO15001 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
Pred. No. 4e-50;
RESULT 467
ID ABO41076 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
Pred. No. 4e-50;
RESULT 468
ID ABO38806 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
Pred. No. 4e-50;
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PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 479
ID ADM312145 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 480
ID ADM32450 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 481
ID ADB68302 standard; protein; 89 AA.
DE Human PRO1069 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 482
ID ADB68109 standard; protein; 89 AA.
DE Human PRO1069 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 483
ID ADM31535 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 484
ID ADM30925 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 485
ID ADB90926 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 486
ID ADC57742 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 487
ID ADC55106 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 488
ID ADC11973 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 489
ID ADC07006 standard; protein; 89 AA.
DE Human PRO1069 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 490
ID ADC56395 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 491
ID ADC17185 standard; protein; 89 AA.
DE Mammalian PRO polypeptide (SeqID 50).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 492
ID ADC07450 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 493
ID ADC11440 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 494
ID ADC14883 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 495
ID ADC52378 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 496
ID ADC14562 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 497
ID ADD08094 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003068623-A1.
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PD 10-APR-2003.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 498  
ID ADC81919 standard; protein; 89 AA.  
DE Human PRO polypeptide #75.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 499  
ID ADD07561 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 500  
ID ADC82452 standard; protein; 89 AA.  
DE Human PRO polypeptide #75.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 501  
ID ADD05673 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 502  
ID ADD08632 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003073090-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 503  
ID ADD06881 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 504  
ID ADC83128 standard; protein; 89 AA.  
DE Human PRO polypeptide #75.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 505  
ID ADD52335 standard; protein; 89 AA.  
DE Human PRO polypeptide #75.  
PN US2003077593-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 506  
ID ADD36054 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003105298-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 507  
ID ADD56193 standard; protein; 89 AA.  
DE Human PRO polypeptide #75.

PN US2003077594-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 508  
ID ADD54631 standard; protein; 89 AA.  
DE Human PRO polypeptide #75.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 509  
ID ADE26785 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 510  
ID ADE26252 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 511  
ID ADF67189 standard; protein; 89 AA.  
DE Human PRO1069 amino acid sequence SEQ ID NO:262.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 512  
ID ADG01055 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003078387-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 513  
ID ADG08608 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 514  
ID ADG02668 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 515  
ID ADG01375 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003207399-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 516  
ID ADF95550 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;

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Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 517
ID ADF95229 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 518
ID ADG12365 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 519
ID ADH24082 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 520
ID ADH34108 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 521
ID ADH29941 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 522
ID ADH23912 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180919-A1.
PD 23-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 523
ID ADH09025 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 524
ID ADG85316 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 525
ID ADH24592 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180907-A1.
PD 23-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 526
ID ADH37788 standard; protein; 89 AA.
DE Human secreted and transmembrane protein PRO1069.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 527
ID ADH02037 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 528
ID ADH37618 standard; protein; 89 AA.
DE Human secreted and transmembrane protein PRO1069.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 529
ID ADG85656 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 530
ID ADH24252 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 531
ID ADH8546 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 532
ID ADG83667 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 533
ID ADH29475 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 534
ID ADH27591 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 535
ID ADH37788 standard; protein; 89 AA.
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DE Human secreted and transmembrane protein PRO1069.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 536  
ID ADH37965 standard; protein; 89 AA.  
DE Human secreted and transmembrane protein PRO1069.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 537  
ID ADH57385 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180920-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 538  
ID ADH53527 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 539  
ID ADH53697 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181641-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 540  
ID ADH52033 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 541  
ID ADH4988 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 542  
ID ADI25398 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 543  
ID ADH90191 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 544  
ID ADI25568 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 545  
ID ADH97742 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 546  
ID ADI35443 standard; protein; 89 AA.  
DE Human PRO polypeptide #75.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 547  
ID ADI03590 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 548  
ID ADI11947 standard; protein; 89 AA.  
DE Human PRO polypeptide #25.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 549  
ID ADH90021 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 550  
ID ADH99935 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 551  
ID ADH98422 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 552  
ID ADI11097 standard; protein; 89 AA.  
DE Human PRO polypeptide #25.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 553  
ID ADI11607 standard; protein; 89 AA.  
DE Human PRO polypeptide #25.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.



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RESULT 572
ID ADI04644 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 582
ID ADI02780 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 583
ID ADH78099 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 584
ID ADI25738 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 585
ID ADI25908 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 586
ID ADK65420 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 587
ID ADH98762 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 588
ID ADH80003 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 589
ID ADL32806 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 590
ID ADM30340 standard; protein; 89 AA.

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DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003073813-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 591  
ID ADL93734 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 592  
ID AD52188 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003130483-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 593  
ID ADE74337 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 594  
ID ADE74949 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #100.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 595  
ID ADF35388 standard; protein; 89 AA.  
DE Human PRO1069 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 596  
ID ADG11638 standard; protein; 89 AA.  
DE Human PRO1069 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 597  
ID ADF96162 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 598  
ID ADG04433 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 599  
ID ADG00593 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 600  
ID ADH06620 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 601  
ID ADH06450 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 602  
ID ADG68871 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 603  
ID ADH27761 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 604  
ID ADH25102 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 605  
ID ADH33734 standard; protein; 89 AA.  
DE Human PRO polypeptide #25.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 606  
ID ADG82849 standard; protein; 89 AA.  
DE Human PRO polypeptide #100.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 607  
ID ADH02377 standard; protein; 89 AA.  
DE Human PRO polypeptide #25.  
PN US2003180839-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 608  
ID ADH07984 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;

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RESULT 609
ID ADG69381 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 8; Length 89;
RESULT 610
ID ADH39202 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 8; Length 89;
RESULT 611
ID ADH26130 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 8; Length 89;
RESULT 612
ID ADG83942 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 8; Length 89;
RESULT 613
ID ADH19508 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 8; Length 89;
RESULT 614
ID ADG85486 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 8; Length 89;
RESULT 615
ID ADH06280 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 8; Length 89;
RESULT 616
ID ADH30110 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 8; Length 89;
RESULT 617
ID ADH24422 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 8; Length 89;
RESULT 618
ID ADH21001 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 8; Length 89;
RESULT 619
ID ADG69551 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 8; Length 89;
RESULT 620
ID ADH07814 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 8; Length 89;
RESULT 621
ID ADG85826 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 8; Length 89;
RESULT 622
ID ADH39372 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 8; Length 89;
RESULT 623
ID ADH33564 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 8; Length 89;
RESULT 624
ID ADH33904 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 8; Length 89;
RESULT 625
ID ADH01114 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 8; Length 89;
RESULT 626
ID ADG69721 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 8; Length 89;
RESULT 627
ID ADH21001 standard; protein; 89 AA.
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DE Human secreted/transmembrane protein PRO1069.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 628  
ID ADH02207 standard; protein; 89 AA.  
DE Human PRO polypeptide #25.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 629  
ID ADG69211 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 630  
ID ADG85996 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180862-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 631  
ID ADH24932 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180909-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 632  
ID ADH39549 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 633  
ID ADH20041 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein PRO1069.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 634  
ID ADH02547 standard; protein; 89 AA.  
DE Human PRO polypeptide #25.  
PN US2003180840-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 635  
ID ADG69041 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180849-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 636  
ID ADH07644 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180850-A1.

PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 637  
ID ADG86166 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180863-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 638  
ID ADH24762 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180908-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 639  
ID ADH25810 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180911-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 640  
ID ADH38376 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180922-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 641  
ID ADH57215 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181642-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 642  
ID ADH52203 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180921-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 643  
ID ADH49569 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003180857-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 644  
ID ADH90531 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO1069.  
PN US2003181700-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 461; DB 8; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4e-50;  
RESULT 645  
ID ADI11267 standard; protein; 89 AA.  
DE Human PRO polypeptide #25.  
PN US2003181683-A1.  
PD 25-SEP-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 646
ID ADH98932 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 647
ID ADI02162 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 648
ID ADH90701 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 649
ID ADJ54838 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 650
ID ADJ98576 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 651
ID ADJ98746 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 652
ID ADH78905 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 653
ID ADJ99139 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 654
ID ADJ99309 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 655
ID ADJ98927 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 656
ID ADH79075 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 657
ID ADK00935 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 658
ID ADK14456 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 659
ID ADJ64609 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 660
ID ADM31505 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 661
ID ADM36552 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 662
ID ADM40357 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 663
ID ADM80905 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
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Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 664
ID ADN37965 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
FN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 665
ID ADY77745 standard; protein; 89 AA.
DE Neoplastic disease detection protein PRO1069.
FN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 461; DB 9; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 666
ID AEA38515 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, #143.
FN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 9; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;
RESULT 667
ID AAW92958 standard; protein; 89 AA.
DE Human zsig44 protein.
FN WO9905276-A1.
PD 04-FEB-1999.
PA (ZYMO ) ZYMOGENETICS INC.
Query Match 98.0%; Score 452; DB 2; Length 89;
Best Local Similarity 98.9%; Pred. No. 5.5e-49;
RESULT 668
ID AAM38770 standard; protein; 89 AA.
DE Human polypeptide SEQ ID NO 1915.
FN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 98.0%; Score 452; DB 4; Length 89;
Best Local Similarity 98.9%; Pred. No. 5.5e-49;
RESULT 669
ID ADK14984 standard; protein; 89 AA.
DE Urinary specific protein #90.
FN WO2003057839-A2.
PD 17-JUL-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 98.0%; Score 452; DB 7; Length 89;
Best Local Similarity 98.9%; Pred. No. 5.5e-49;
RESULT 670
ID AAM40556 standard; protein; 117 AA.
DE Human polypeptide SEQ ID NO 5487.
FN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 98.0%; Score 452; DB 4; Length 117;
Best Local Similarity 98.9%; Pred. No. 7.9e-49;
RESULT 671
ID ADP07847 standard; protein; 89 AA.
DE Human secreted protein, seq id 330.
FN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 97.0%; Score 447; DB 8; Length 89;
Best Local Similarity 97.8%; Pred. No. 2.4e-48;

RESULT 672
ID ADN38992 standard; protein; 186 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:210.
FN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 81.1%; Score 374; DB 7; Length 186;
Best Local Similarity 94.7%; Pred. No. 1.1e-38;
RESULT 673
ID ADN38994 standard; protein; 318 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:212.
FN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 81.1%; Score 374; DB 7; Length 318;
Best Local Similarity 94.7%; Pred. No. 2.2e-38;
RESULT 674
ID AAE05362 standard; protein; 88 AA.
DE Mouse channel inducing factor precursor (CHIF) protein.
FN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 60.0%; Score 276.5; DB 4; Length 88;
Best Local Similarity 66.7%; Pred. No. 9.7e-27;
RESULT 675
ID ABB72374 standard; protein; 88 AA.
DE Murine protein isolated from skin cells SEQ ID NO: 698.
FN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 60.0%; Score 276.5; DB 5; Length 88;
Best Local Similarity 66.7%; Pred. No. 9.7e-27;
RESULT 676
ID AAW92966 standard; protein; 87 AA.
DE Rat CHIF protein.
FN WO9905276-A1.
PD 04-FEB-1999.
PA (ZYMO ) ZYMOGENETICS INC.
Query Match 55.6%; Score 256.5; DB 2; Length 87;
Best Local Similarity 61.5%; Pred. No. 3.3e-24;
RESULT 677
ID AAR90991 standard; protein; 88 AA.
DE Mouse Mat-8 polypeptide.
FN WO9605322-A1.
PD 22-FEB-1996.
PA (GEHO ) GEN HOSPITAL CORP.
PA (HARD ) HARVARD COLLEGE.
Query Match 52.4%; Score 241.5; DB 2; Length 88;
Best Local Similarity 57.8%; Pred. No. 2.7e-22;
RESULT 678
ID AAR90990 standard; protein; 87 AA.
DE Human Mat-8 polypeptide.
FN WO9605322-A1.
PD 22-FEB-1996.
PA (GEHO ) GEN HOSPITAL CORP.
PA (HARD ) HARVARD COLLEGE.
Query Match 46.5%; Score 214.5; DB 2; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 679
ID AAY48304 standard; protein; 87 AA.
DE Human prostate cancer-associated protein 1.
FN DE19811194-A1.
PD 16-SEP-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 46.5%; Score 214.5; DB 2; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 680
ID AAW92959 standard; protein; 87 AA.
DE Human MAT-8 protein.
FN WO9905276-A1.
PD 04-FEB-1999.
PA (ZYMO ) ZYMOGENETICS INC.
Query Match 46.5%; Score 214.5; DB 2; Length 87;
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Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 681
ID AAM23962 standard; protein; 87 AA.
DE Human EST encoded protein SEQ ID NO: 1487.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 46.5%; Score 214.5; DB 4; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 682
ID ABJ37036 standard; protein; 87 AA.
DE Human breast cancer / ovarian cancer related protein #12.
PN WO2003000012-A2.
PD 03-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 46.5%; Score 214.5; DB 6; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 683
ID ABR47467 standard; protein; 87 AA.
DE Breast cancer associated protein sequence SEQ ID NO:166.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 46.5%; Score 214.5; DB 6; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 684
ID ABP75985 standard; protein; 87 AA.
DE Human GENSET protein SEQ ID 192.
PN WO200283898-A1.
PD 24-OCT-2002.
PA (GEST-) GENSET.
Query Match 46.5%; Score 214.5; DB 6; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 685
ID ABP76150 standard; protein; 87 AA.
DE Human GENSET protein SEQ ID 476.
PN WO200283898-A1.
PD 24-OCT-2002.
PA (GEST-) GENSET.
Query Match 46.5%; Score 214.5; DB 6; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 686
ID ADB75316 standard; protein; 87 AA.
DE Prostate cancer marker protein.
PN WO2003009814-A2.
PD 06-FEB-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 46.5%; Score 214.5; DB 7; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 687
ID ADN40040 standard; protein; 87 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C410.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 46.5%; Score 214.5; DB 7; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 688
ID ADI36718 standard; protein; 87 AA.
DE Human PML #2.
PN US2003225014-A1.
PD 04-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 46.5%; Score 214.5; DB 8; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 689
ID ADK70447 standard; protein; 87 AA.
DE Respiratory disease differentially expressed protein #13.
PN WO2003101283-A2.
PD 11-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 46.5%; Score 214.5; DB 8; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 690
ID ADQ80368 standard; protein; 87 AA.
DE FYXD domain containing ion transport regulator 3 protein.
PN WO2004063709-A2.
PD 23-JUL-2004.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match 46.5%; Score 214.5; DB 8; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 691
ID ADZ69596 standard; protein; 87 AA.
DE Human phospholemman-like protein (PLML) SEQ ID NO:10.
PN US2005101558-A1.
PD 12-MAY-2005.
PA (WATT-) WATT A T.
Query Match 46.5%; Score 214.5; DB 9; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 692
ID AEB29726 standard; protein; 87 AA.
DE Human FYXD domain-containing ion transport regulator 3.
PN WO2005067667-A2.
PD 28-JUL-2005.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match 46.5%; Score 214.5; DB 9; Length 87;
Best Local Similarity 54.5%; Pred. No. 6.9e-19;
RESULT 693
ID ABJ19334 standard; protein; 116 AA.
DE NOVX related protein SEQ ID No 34.
PN WO200299062-A2.
PD 12-DEC-2002.
PA (CURA-) CURAGEN CORP.
Query Match 46.5%; Score 214.5; DB 6; Length 116;
Best Local Similarity 54.5%; Pred. No. 1e-18;
RESULT 694
ID ADQ41668 standard; protein; 116 AA.
DE Novel human polypeptide NOV13b.
PN US2004018555-A1.
PD 29-JAN-2004.
PA (ANDE-) ANDERSON D W.
PA (ZERH-) ZERHUSEN B D.
PA (LILL-) LI L.
PA (ZHON-) ZHONG M.
PA (CASM-) CASMAN S J.
PA (GERL-) GERLACH V.
PA (SHIM-) SHIMKETS R A.
PA (GORM-) GORMAN L.
PA (PENA-) PENA C E A.
PA (KEKU-) KEKUDA R.
PA (PATT-) PATTURAJAN M.
PA (SPYT-) SPYTEK K A.
PA (LEIT-) LEITE M W.
PA (RAST-) RASTELLI L.
PA (MACD-) MACDOUGALL J R.
PA (TAUP-) TAUPIER R J.
PA (GUOX-) GUO X S.
PA (MILL-) MILLER C E.
PA (SHEN-) SHENOY S G.
PA (HJAL-) HJALT T.
PA (VOSS-) VOSS B Z.
PA (BOLD-) BOLDOG F L.
PA (MADY-) MARYANKAR U M.
PA (PADI-) PADIGARU M.
PA (JIWW-) JI W.
PA (SMIT-) SMITHSON G.
PA (EDIN-) EDINGER S R.
PA (MILL-) MILLET I.
PA (ELLE-) ELLERMAN K.
Query Match 46.5%; Score 214.5; DB 8; Length 116;
Best Local Similarity 54.5%; Pred. No. 1e-18;
RESULT 695
ID ABJ19333 standard; protein; 86 AA.
DE NOVX related protein SEQ ID No 32.
PN WO200299062-A2.
PD 12-DEC-2002.

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PA (CURA-) CURAGEN CORP.  
Query Match 45.4%; Score 209.5; DB 6; Length 86;  
Best Local Similarity 54.0%; Pred. No. 2.9e-18;  
RESULT 696  
ID ADO41666 standard; protein; 86 AA.  
DE Novel human polypeptide NOV13a.  
PN US2004018555-A1.  
PD 29-JAN-2004.  
PA (ANDE/) ANDERSON D W.  
PA (ZERH/) ZERHUSEN B D.  
PA (LILL/) LI L.  
PA (ZHON/) ZHONG M.  
PA (CASM/) CASMAN S J.  
PA (GERL/) GERLACH V.  
PA (SHIM/) SHIMKETS R A.  
PA (GORM/) GORMAN L.  
PA (PENI/) PENA C E A.  
PA (KEKU/) KEKUDA R.  
PA (PATT/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (LEIT/) LEITE M W.  
PA (RAST/) RASTELLI L.  
PA (MACD/) MACDOUGALL J R.  
PA (TAUP/) TAUPIER R J.  
PA (GUOX/) GUO X S.  
PA (MILL/) MILLER C E.  
PA (SHEN/) SHENOY S G.  
PA (HUAL/) HUALT T.  
PA (BOSS/) BOSS E Z.  
PA (BOLD/) BOLDOG F L.  
PA (MALV/) MALYANKAR U M.  
PA (PADJ/) PADIGARU M.  
PA (JIWW/) JI W.  
PA (SMIT/) SMITHSON G.  
PA (EDIN/) EDINGER S R.  
PA (MILL/) MILLET I.  
PA (ELLE/) ELLERMAN K.  
Query Match 45.4%; Score 209.5; DB 8; Length 86;  
Best Local Similarity 54.0%; Pred. No. 2.9e-18;  
RESULT 697  
ID ABR47468 standard; protein; 113 AA.  
DE Breast cancer associated protein sequence SEQ ID NO:168.  
PN WO2003004989-A2.  
PD 16-JAN-2003.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 41.5%; Score 191.5; DB 6; Length 113;  
Best Local Similarity 42.1%; Pred. No. 8e-16;  
RESULT 698  
ID ADB75318 standard; protein; 113 AA.  
DE Prostate cancer marker protein.  
PN WO2003009814-A2.  
PD 06-FEB-2003.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 41.5%; Score 191.5; DB 7; Length 113;  
Best Local Similarity 42.1%; Pred. No. 8e-16;  
RESULT 699  
ID ADN40039 standard; protein; 113 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C409.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 41.5%; Score 191.5; DB 7; Length 113;  
Best Local Similarity 42.1%; Pred. No. 8e-16;  
RESULT 700  
ID AAB53415 standard; protein; 150 AA.  
DE Human colon cancer antigen protein sequence SEQ ID NO:955.  
PN WO200055351-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.5%; Score 191.5; DB 3; Length 150;  
Best Local Similarity 42.1%; Pred. No. 1.2e-15;  
RESULT 701  
ID ADI36717 standard; protein; 111 AA.

DE Human PLML #1.  
PN US2003225014-A1.  
PD 04-DEC-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 38.1%; Score 175.5; DB 8; Length 111;  
Best Local Similarity 41.2%; Pred. No. 8.3e-14;  
RESULT 702  
ID ADZ69595 standard; protein; 111 AA.  
DE Human phospholemmann-like protein (PLML) SEQ ID NO:3.  
PN US2005101558-A1.  
PD 12-MAY-2005.  
PA (WATT/) WATT A T.  
Query Match 38.1%; Score 175.5; DB 9; Length 111;  
Best Local Similarity 41.2%; Pred. No. 8.3e-14;  
RESULT 703  
ID ABG75841 standard; protein; 67 AA.  
DE Transporters and ion channels protein 23, TRICH-23.  
PN WO2003016493-A2.  
PD 27-FEB-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 32.5%; Score 150; DB 6; Length 67;  
Best Local Similarity 56.6%; Pred. No. 7.4e-11;  
RESULT 704  
ID ABUS2799 standard; protein; 83 AA.  
DE Human signal transduction-associated DKF7phfbr2\_92i17 homologue.  
PN WO200112659-A2.  
PD 22-FEB-2001.  
PA (GERU-) GERMAN HUMAN GENOME PROJECT.  
Query Match 28.0%; Score 129; DB 4; Length 83;  
Best Local Similarity 41.3%; Pred. No. 4.5e-08;  
RESULT 705  
ID AAW75161 standard; protein; 92 AA.  
DE Human secreted protein encoded by gene 50 clone HHSZ57.  
PN WO9839446-A2.  
PD 11-SEP-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 28.0%; Score 129; DB 2; Length 92;  
Best Local Similarity 41.3%; Pred. No. 5.1e-08;  
RESULT 706  
ID AAY24749 standard; protein; 92 AA.  
DE Human phospholemmann homologue protein.  
PN US5919655-A.  
PD 06-JUL-1999.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 28.0%; Score 129; DB 2; Length 92;  
Best Local Similarity 41.3%; Pred. No. 5.1e-08;  
RESULT 707  
ID AAY59689 standard; protein; 92 AA.  
DE Secreted protein 26-44-1-B5-CL3\_1.  
PN WO940189-A2.  
PD 12-AUG-1999.  
PA (GEST-) GENSET.  
Query Match 28.0%; Score 129; DB 2; Length 92;  
Best Local Similarity 41.3%; Pred. No. 5.1e-08;  
RESULT 708  
ID AAY48331 standard; protein; 92 AA.  
DE Human prostate cancer-associated protein 28.  
PN DE19811194-A1.  
PD 16-SEP-1999.  
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.  
Query Match 28.0%; Score 129; DB 2; Length 92;  
Best Local Similarity 41.3%; Pred. No. 5.1e-08;  
RESULT 709  
ID AAW92960 standard; protein; 92 AA.  
DE Human PLM protein.  
PN WO9905276-A1.  
PD 04-FEB-1999.  
PA (ZYMO-) ZYMOGENETICS INC.  
Query Match 28.0%; Score 129; DB 2; Length 92;  
Best Local Similarity 41.3%; Pred. No. 5.1e-08;  
RESULT 710  
ID ABB97244 standard; protein; 92 AA.  
DE Novel human protein SEQ ID NO: 512.

PN WO200222660-A2.  
 PD 21-MAR-2002  
 PA (HYSE-) HYSEQ INC.  
 Query Match 28.0%; Score 129; DB 5; Length 92;  
 Best Local Similarity 41.3%; Pred. No. 5.1e-08;  
 RESULT 711  
 ID ABO02037 standard; protein; 92 AA.  
 DE Novel human secreted protein #105.  
 PN US2003027132-A1.  
 PD 06-FEB-2003.  
 PA (RUBE/) RUBEN S M.  
 PA (ROSE/) ROSEN C A.  
 PA (FISC/) FISCHER C L.  
 PA (SOPP/) SOPPET D R.  
 PA (CART/) CARTER K C.  
 PA (BEDN/) BEDNARIK D R.  
 PA (ENDR/) ENDRESS G A.  
 PA (YUGG/) YU G.  
 PA (NIJJ/) NI J.  
 PA (FENG/) FENG P E.  
 PA (YOUN/) YOUNG P E.  
 PA (GREE/) GREENE J M.  
 PA (FERR/) FERRIE A M.  
 PA (DUAN/) DUAN R.  
 PA (HUJJ/) HU J.  
 PA (FLOR/) FLORENCE K A.  
 PA (OLSE/) OLSEN H S.  
 PA (EBNE/) EBNER R.  
 PA (BREW/) BREWER L A.  
 PA (SHIV/) SHI Y.  
 Query Match 28.0%; Score 129; DB 6; Length 92;  
 Best Local Similarity 41.3%; Pred. No. 5.1e-08;  
 RESULT 712  
 ID ADE58521 standard; protein; 92 AA.  
 DE Human Protein O00168, SEQ ID NO 4396.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO) GEN HOSPITAL CORP.  
 PA (FARB) BAYER AG.  
 Query Match 28.0%; Score 129; DB 7; Length 92;  
 Best Local Similarity 41.3%; Pred. No. 5.1e-08;  
 RESULT 713  
 ID ADE58525 standard; protein; 92 AA.  
 DE Human Protein O00168, SEQ ID NO 4400.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO) GEN HOSPITAL CORP.  
 PA (FARB) BAYER AG.  
 Query Match 28.0%; Score 129; DB 7; Length 92;  
 Best Local Similarity 41.3%; Pred. No. 5.1e-08;  
 RESULT 714  
 ID ADE83505 standard; protein; 92 AA.  
 DE Human Protein O00168, SEQ ID NO 11101.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO) GEN HOSPITAL CORP.  
 PA (FARB) BAYER AG.  
 Query Match 28.0%; Score 129; DB 7; Length 92;  
 Best Local Similarity 41.3%; Pred. No. 5.1e-08;  
 RESULT 715  
 ID ADJ69464 standard; protein; 92 AA.  
 DE Human heat mitochondrial protein as a therapeutic target SeqID1270.  
 PN WO2003087768-A2.  
 PD 23-OCT-2003.  
 PA (MITO-) MITOKOR.  
 PA (BUCK-) BUCK INST AGE RES.  
 Query Match 28.0%; Score 129; DB 7; Length 92;  
 Best Local Similarity 41.3%; Pred. No. 5.1e-08;  
 RESULT 716  
 ID ADM77839 standard; protein; 92 AA.  
 DE Human protein #36.  
 PN US2003162176-A1.  
 PD 28-AUG-2003.

PA (EDWA/) EDWARDS J D M.  
 PA (DUCL/) DUCLERT A.  
 PA (BOUG/) BOUGUELERET L.  
 Query Match 28.0%; Score 129; DB 7; Length 92;  
 Best Local Similarity 41.3%; Pred. No. 5.1e-08;  
 RESULT 717  
 ID ADN05844 standard; protein; 92 AA.  
 DE Antipeoriatic protein sequence #1085.  
 PN WO2004028479-A2.  
 PD 08-APR-2004.  
 PA (GETH) GENENTECH INC.  
 Query Match 28.0%; Score 129; DB 8; Length 92;  
 Best Local Similarity 41.3%; Pred. No. 5.1e-08;  
 RESULT 718  
 ID ADP19520 standard; protein; 92 AA.  
 DE Human secreted polypeptide #371.  
 PN US2004110939-A1.  
 PD 10-JUN-2004.  
 PA (GEST) GENSET SA.  
 Query Match 28.0%; Score 129; DB 8; Length 92;  
 Best Local Similarity 41.3%; Pred. No. 5.1e-08;  
 RESULT 719  
 ID ADZ12438 standard; protein; 92 AA.  
 DE Human secreted protein sequence encoded by gene 50 SEQ ID NO:238.  
 PN US6878687-B1.  
 PD 12-APR-2005.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 28.0%; Score 129; DB 9; Length 92;  
 Best Local Similarity 41.3%; Pred. No. 5.1e-08;  
 RESULT 720  
 ID ADZ89299 standard; protein; 92 AA.  
 DE Secreted protein encoded by extended EST cDNA #36.  
 PN US2005106599-A1.  
 PD 19-MAY-2005.  
 PA (EDWA/) EDWARDS J D M.  
 PA (DUCL/) DUCLERT A.  
 PA (BOUG/) BOUGUELERET L.  
 Query Match 28.0%; Score 129; DB 9; Length 92;  
 Best Local Similarity 41.3%; Pred. No. 5.1e-08;  
 RESULT 721  
 ID AAW75106 standard; protein; 93 AA.  
 DE Human secreted protein encoded by gene 50 clone HHSZ57.  
 PN WO9839446-A2.  
 PD 11-SEP-1998.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 28.0%; Score 129; DB 2; Length 93;  
 Best Local Similarity 41.3%; Pred. No. 5.2e-08;  
 RESULT 722  
 ID ABO01982 standard; protein; 93 AA.  
 DE Novel human secreted protein #50.  
 PN US2003027132-A1.  
 PD 06-FEB-2003.  
 PA (RUBE/) RUBEN S M.  
 PA (ROSE/) ROSEN C A.  
 PA (FISC/) FISCHER C L.  
 PA (SOPP/) SOPPET D R.  
 PA (CART/) CARTER K C.  
 PA (BEDN/) BEDNARIK D R.  
 PA (ENDR/) ENDRESS G A.  
 PA (YUGG/) YU G.  
 PA (NIJJ/) NI J.  
 PA (FENG/) FENG P E.  
 PA (YOUN/) YOUNG P E.  
 PA (GREE/) GREENE J M.  
 PA (FERR/) FERRIE A M.  
 PA (DUAN/) DUAN R.  
 PA (HUJJ/) HU J.  
 PA (FLOR/) FLORENCE K A.  
 PA (OLSE/) OLSEN H S.  
 PA (EBNE/) EBNER R.  
 PA (BREW/) BREWER L A.  
 PA (SHIV/) SHI Y.  
 Query Match 28.0%; Score 129; DB 6; Length 93;

Best Local Similarity 41.3%; Pred. No. 5.2e-08;  
RESULT 723  
ID ADZ12383 standard; protein; 93 AA.  
DE Human secreted protein sequence encoded by gene 50 SEQ ID NO:183.  
PN US6878687-B1.  
PD 12-APR-2005.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 28.0%; Score 129; DB 9; Length 93;  
Best Local Similarity 41.3%; Pred. No. 5.2e-08;  
RESULT 724  
ID ABO02067 standard; protein; 70 AA.  
DE Novel human secreted protein associated protein fragment #12.  
PN US2003027132-A1.  
PD 06-FEB-2003.  
PA (RUBE/) RUBEN S M.  
PA (ROSE/) ROSEN C A.  
PA (FISC/) FISCHER C L.  
PA (SOPP/) SOPPET D R.  
PA (CART/) CARTER K C.  
PA (BEDN/) BEDNARIK D R.  
PA (ENDR/) ENDRESS G A.  
PA (YUGG/) YU G.  
PA (NIJJ/) NI J.  
PA (FENG/) FENG P.  
PA (YOUN/) YOUNG P E.  
PA (GREE/) GREENE J M.  
PA (FERR/) FERRIE A M.  
PA (DUAN/) DUAN R.  
PA (HUJU/) HU J.  
PA (FLOR/) FLORENCE K A.  
PA (OLSE/) OLSEN H S.  
PA (EBNE/) EBNER R.  
PA (BREW/) BREWER L A.  
PA (SHIY/) SHI Y.  
Query Match 26.2%; Score 121; DB 6; Length 70;  
Best Local Similarity 44.9%; Pred. No. 3.7e-07;  
RESULT 725  
ID ADZ12469 standard; protein; 70 AA.  
DE Human gene 50 secreted protein related sequence SEQ ID NO:269.  
PN US6878687-B1.  
PD 12-APR-2005.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 26.2%; Score 121; DB 9; Length 70;  
Best Local Similarity 44.9%; Pred. No. 3.7e-07;  
RESULT 726  
ID AAY12377 standard; protein; 63 AA.  
DE Human 5' EST secreted protein SEQ ID NO:408.  
PN WO9906548-A2.  
PD 11-FEB-1999.  
PA (GEST/) GENSET.  
Query Match 24.7%; Score 114; DB 2; Length 63;  
Best Local Similarity 43.1%; Pred. No. 2.5e-06;  
RESULT 727  
ID ADE58523 standard; protein; 92 AA.  
DE Rat Protein O08589, SEQ ID NO 4398.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO/) GEN HOSPITAL CORP.  
PA (FARB/) BAYER AG.  
Query Match 24.7%; Score 114; DB 7; Length 92;  
Best Local Similarity 31.6%; Pred. No. 4.1e-06;  
RESULT 728  
ID ADE58519 standard; protein; 92 AA.  
DE Rat Protein O08589, SEQ ID NO 4394.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO/) GEN HOSPITAL CORP.  
PA (FARB/) BAYER AG.  
Query Match 24.7%; Score 114; DB 7; Length 92;  
Best Local Similarity 31.6%; Pred. No. 4.1e-06;  
RESULT 729  
ID ADE83503 standard; protein; 92 AA.  
DE Rat Protein O08589, SEQ ID NO 11099.

PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO/) GEN HOSPITAL CORP.  
PA (FARB/) BAYER AG.  
Query Match 24.7%; Score 114; DB 7; Length 92;  
Best Local Similarity 31.6%; Pred. No. 4.1e-06;  
RESULT 730  
ID AAM38777 standard; protein; 138 AA.  
DE Human polypeptide SEQ ID NO 1922.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 24.6%; Score 113.5; DB 4; Length 138;  
Best Local Similarity 34.2%; Pred. No. 8e-06;  
RESULT 731  
ID AAU14339 standard; protein; 138 AA.  
DE Human novel protein #210.  
PN WO200155437-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 24.6%; Score 113.5; DB 4; Length 138;  
Best Local Similarity 34.2%; Pred. No. 8e-06;  
RESULT 732  
ID AAM40563 standard; protein; 155 AA.  
DE Human polypeptide SEQ ID NO 5494.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 24.6%; Score 113.5; DB 4; Length 155;  
Best Local Similarity 34.2%; Pred. No. 9.3e-06;  
RESULT 733  
ID AAW51104 standard; protein; 95 AA.  
DE A human phospholemmann-like protein.  
PN WO9814572-A1.  
PD 09-APR-1998.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 24.4%; Score 112.5; DB 2; Length 95;  
Best Local Similarity 36.0%; Pred. No. 6.6e-06;  
RESULT 734  
ID AAU14575 standard; protein; 95 AA.  
DE Human novel protein #446.  
PN WO200155437-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 24.4%; Score 112.5; DB 4; Length 95;  
Best Local Similarity 36.0%; Pred. No. 6.6e-06;  
RESULT 735  
ID ABUS2798 standard; protein; 95 AA.  
DE Human signal transduction-associated protein from DKFZphfbr2\_82i17.  
PN WO200112659-A2.  
PD 22-FEB-2001.  
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
Query Match 24.4%; Score 112.5; DB 4; Length 95;  
Best Local Similarity 36.0%; Pred. No. 6.6e-06;  
RESULT 736  
ID ADH80893 standard; protein; 95 AA.  
DE Human polypeptide #210.  
PN US2003232054-A1.  
PD 18-DEC-2003.  
PA (TANG/) TANG Y T.  
PA (LIUC/) LIU C.  
PA (ASUN/) ASUNDI V.  
PA (CHEN/) CHEN R.  
PA (QIAN/) QIAN X B.  
PA (WANG/) WANG Z W.  
PA (WEHR/) WEHRMAN T.  
PA (ZHAN/) ZHANG J.  
PA (ZHOU/) ZHOU P.  
PA (CAOY/) CAO Y.  
PA (DRMA/) DRMANAC R T.  
Query Match 24.4%; Score 112.5; DB 8; Length 95;  
Best Local Similarity 36.0%; Pred. No. 6.6e-06;  
RESULT 737

ID ABM81305 standard; protein; 95 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO82051, SEQ:3370.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 95;  
Best Local Similarity 36.0%; Pred. No. 6.6e-06;  
RESULT 738  
ID AAW74882 standard; protein; 96 AA.  
DE Human secreted protein encoded by gene 154 clone H56FL83.  
PN WO9839448-A2.  
PD 11-SEP-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 24.4%; Score 112.5; DB 2; Length 96;  
Best Local Similarity 36.0%; Pred. No. 6.7e-06;  
RESULT 739  
ID ABG95333 standard; protein; 96 AA.  
DE Human novel secreted protein #154.  
PN US6420526-B1.  
PD 16-JUL-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 24.4%; Score 112.5; DB 5; Length 96;  
Best Local Similarity 36.0%; Pred. No. 6.7e-06;  
RESULT 740  
ID ABO34527 standard; protein; 96 AA.  
DE Region of human secreted protein encoded by cDNA sequence #154.  
PN US2003049618-A1.  
PD 13-MAR-2003.  
PA (RUBE/) RUBEN S M.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (CART/) CARTER K C.  
PA (BEDN/) BEDNARIK D P.  
PA (ENDR/) ENDRESS G A.  
PA (YUGG/) YU G.  
PA (NIJJ/) NI J.  
PA (FENG/) FENG P.  
PA (YOUN/) YOUNG P E.  
PA (GREE/) GREENE J M.  
PA (FERR/) FERRIE A M.  
PA (DUAN/) DUAN D R.  
PA (HUJU/) HU J.  
PA (FLOR/) FLORENCE K A.  
PA (OLSE/) OLSEN H S.  
PA (FISC/) FISCHER C L.  
PA (EBNE/) EBNER R.  
PA (BREW/) BREWER L A.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (LAFL/) LAFLEUR D W.  
PA (LIYY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (KYAW/) KYAW H.  
Query Match 24.4%; Score 112.5; DB 6; Length 96;  
Best Local Similarity 36.0%; Pred. No. 6.7e-06;  
RESULT 741  
ID ADI23188 standard; protein; 96 AA.  
DE Novel human secreted protein seq id 473.  
PN US2003175858-A1.  
PD 18-SEP-2003.  
PA (RUBE/) RUBEN S M.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (CART/) CARTER K C.  
PA (BEDN/) BEDNARIK D P.  
PA (ENDR/) ENDRESS G A.  
PA (YUGG/) YU G.  
PA (NIJJ/) NI J.  
PA (FENG/) FENG P.  
PA (YOUN/) YOUNG P E.  
PA (GREE/) GREENE J M.  
PA (FERR/) FERRIE A M.  
PA (DUAN/) DUAN D R.

PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 750  
ID ABUS8949 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein, #77.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 751  
ID ABU60527 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein, #77.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 752  
ID ABU13909 standard; protein; 120 AA.  
DE Human PRO1056 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 753  
ID ABU81086 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003043111-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 754  
ID ABU72494 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 755  
ID ABU66786 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 756  
ID ABUS9867 standard; protein; 120 AA.  
DE Novel secreted and transmembrane protein PRO1056.  
PN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 757  
ID ABO25940 standard; protein; 120 AA.  
DE Human PRO1056 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 758  
ID ABO25057 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein (PRO) #217.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 759  
ID ABUS8949 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein, #77.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 760  
ID ABU92327 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 761  
ID ABUS9392 standard; protein; 120 AA.  
DE Novel human secreted or transmembrane protein PRO826.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 762  
ID ABU67062 standard; protein; 120 AA.  
DE Human secreted/transmembrane, PRO, protein SEQ ID 434.  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 763  
ID ABU92158 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 764  
ID ABU10864 standard; protein; 120 AA.  
DE Human PRO polypeptide #50.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 765  
ID ABU81616 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 766  
ID ABU88555 standard; protein; 120 AA.  
DE Human secreted and transmembrane polypeptide PRO1056.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 767  
ID ABO34069 standard; protein; 120 AA.  
DE Human PRO1056 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 768  
ID ADA45953 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003022328-A1.

PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 769  
ID ADA76384 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 770  
ID ADA19034 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 771  
ID ADA61657 standard; protein; 120 AA.  
DE Homo sapiens.  
PN US2003049816-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 772  
ID ADB19442 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 773  
ID ADB27983 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 774  
ID ADA86462 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 775  
ID ADB16026 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003087350-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 776  
ID ADA37710 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein PRO1056.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 777  
ID ADA47812 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 778  
ID ADA21396 standard; protein; 120 AA.  
DE Human secreted/transmembrane polypeptide PRO1056.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 779  
ID ADA10183 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein, PRO1056.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 780  
ID ADA67607 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 781  
ID ADB30614 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003068794-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 782  
ID ADA85910 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 783  
ID ADA17727 standard; protein; 120 AA.  
DE Human PRO1056 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 784  
ID ADA97122 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 785  
ID ADA79426 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 786  
ID ADA87565 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 787  
ID ADA47812 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003073215-A1.  
PD 17-APR-2003.

ID	ADB16767 standard; protein; 120 AA.
DE	Human PRO polypeptide #217.
PN	US2003087349-A1.
PD	08-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity	36.0%; Pred. No. 9e-06;
RESULT 788	
ID	ADA27835 standard; protein; 120 AA.
DE	Human secreted/transmembrane protein PRO1056.
PN	US2003054359-A1.
PD	20-MAR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity	36.0%; Pred. No. 9e-06;
RESULT 789	
ID	ADA91859 standard; protein; 120 AA.
DE	Novel human secreted and transmembrane protein PRO1056.
PN	US2003082694-A1.
PD	01-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity	36.0%; Pred. No. 9e-06;
RESULT 790	
ID	ADB14922 standard; protein; 120 AA.
DE	Human PRO polypeptide #217.
PN	US2003087351-A1.
PD	08-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity	36.0%; Pred. No. 9e-06;
RESULT 791	
ID	ADB18883 standard; protein; 120 AA.
DE	Novel human secreted and transmembrane protein PRO1056.
PN	US2003073211-A1.
PD	17-APR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity	36.0%; Pred. No. 9e-06;
RESULT 792	
ID	ADA94098 standard; protein; 120 AA.
DE	Human PRO polypeptide #217.
PN	US2003077722-A1.
PD	24-APR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity	36.0%; Pred. No. 9e-06;
RESULT 793	
ID	ADB19994 standard; protein; 120 AA.
DE	Novel human secreted and transmembrane protein PRO1056.
PN	US2003082691-A1.
PD	01-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity	36.0%; Pred. No. 9e-06;
RESULT 794	
ID	ADB13306 standard; protein; 120 AA.
DE	Human PRO polypeptide #217.
PN	US2003082710-A1.
PD	01-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity	36.0%; Pred. No. 9e-06;
RESULT 795	
ID	AEO43365 standard; protein; 120 AA.
DE	Novel human secreted and transmembrane protein PRO1056.
PN	US2003044945-A1.
PD	06-MAR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity	36.0%; Pred. No. 9e-06;
RESULT 796	
ID	ADA94415 standard; protein; 120 AA.
DE	Human secreted/transmembrane protein PRO1056.
PN	US2003082703-A1.
PD	01-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity	36.0%; Pred. No. 9e-06;
RESULT 797	
ID	ADA75832 standard; protein; 120 AA.
DE	Human PRO polypeptide #217.
PN	US2003082703-A1.
PD	01-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity	36.0%; Pred. No. 9e-06;
RESULT 798	
ID	ADB24793 standard; protein; 120 AA.
DE	Human PRO polypeptide SEQ ID NO 434.
PN	US2003077713-A1.
PD	24-APR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity	36.0%; Pred. No. 9e-06;
RESULT 799	
ID	ADA82317 standard; protein; 120 AA.
DE	Human PRO polypeptide #217.
PN	US2003082701-A1.
PD	01-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity	36.0%; Pred. No. 9e-06;
RESULT 800	
ID	ADA75280 standard; protein; 120 AA.
DE	Human PRO polypeptide #217.
PN	US2003073216-A1.
PD	17-APR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity	36.0%; Pred. No. 9e-06;
RESULT 801	
ID	ADA85358 standard; protein; 120 AA.
DE	Novel human secreted and transmembrane protein PRO1056.
PN	US2003082695-A1.
PD	01-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity	36.0%; Pred. No. 9e-06;
RESULT 802	
ID	ADA84806 standard; protein; 120 AA.
DE	Novel human secreted and transmembrane protein PRO1056.
PN	US2003082708-A1.
PD	01-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity	36.0%; Pred. No. 9e-06;
RESULT 803	
ID	ADB30062 standard; protein; 120 AA.
DE	Human PRO polypeptide #217.
PN	US2003073214-A1.
PD	17-APR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity	36.0%; Pred. No. 9e-06;
RESULT 804	
ID	ADA80590 standard; protein; 120 AA.
DE	Human PRO polypeptide #217.
PN	US2003082761-A1.
PD	01-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity	36.0%; Pred. No. 9e-06;
RESULT 805	
ID	



PA (GETH ) GENENTECH INC. 24.4%; Score 112.5; DB 6; Length 120;  
Query Match 36.0%; Pred. No. 9e-06;  
RESULT 806  
ID ADA38640 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein PRO1056.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 807  
ID ADA47057 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003073210-A1.  
PD 17-APR-2003.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 808  
ID ADA96018 standard; protein; 120 AA.  
DE Human PRO polypeptide SEQ ID NO 434.  
PN US2003077715-A1.  
PD 24-APR-2003.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 809  
ID ADA93529 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003077721-A1.  
PD 24-APR-2003.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 810  
ID ADB26879 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003092147-A1.  
PD 15-MAY-2003.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 811  
ID ADB31166 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003096386-A1.  
PD 22-MAY-2003.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 812  
ID ADA92761 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein PRO1056.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 813  
ID ADA61094 standard; protein; 120 AA.  
DE Homo sapiens.  
PN US2003049817-A1.  
PD 13-MAR-2003.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 814  
ID ADB24241 standard; protein; 120 AA.  
DE Human PRO polypeptide SEQ ID NO 434.  
PN US2003077714-A1.  
PD 24-APR-2003.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;

RESULT 815  
ID ADA96570 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003082690-A1.  
PD 01-MAY-2003.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 816  
ID ADA81142 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003082702-A1.  
PD 01-MAY-2003.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 817  
ID ADA96018 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003082759-A1.  
PD 01-MAY-2003.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 818  
ID ADB26327 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003082760-A1.  
PD 01-MAY-2003.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 819  
ID ADB21812 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003082765-A1.  
PD 01-MAY-2003.  
Query Match 24.4%; Score 112.5; DB 6; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 820  
ID ADA77591 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003068797-A1.  
PD 10-APR-2003.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 821  
ID ADB18331 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003077710-A1.  
PD 24-APR-2003.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 822  
ID ADA87014 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 823  
ID ADA88117 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003082700-A1.  
PD 01-MAY-2003.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 824  
ID ADA88117 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003082700-A1.  
PD 01-MAY-2003.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;

[illegible]

DE Human PRO polypeptide #50.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 844  
ID ADB38174 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003087347-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 845  
ID ADB6646 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003082689-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 846  
ID ADB89726 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003082698-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 847  
ID ADB90458 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003082762-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 848  
ID ADB39559 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003082764-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 849  
ID ADB47182 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 850  
ID ADB86789 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003082697-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 851  
ID ADB77394 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003082696-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 852  
ID ADB34551 standard; protein; 120 AA.  
DE Human PRO polypeptide SEQ ID NO 434.  
PN US2003077717-A1.

PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 853  
ID ADB35655 standard; protein; 120 AA.  
DE Human PRO polypeptide SEQ ID NO 434.  
PN US2003077719-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 854  
ID ADB33999 standard; protein; 120 AA.  
DE Human PRO polypeptide SEQ ID NO 434.  
PN US2003077716-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 855  
ID ADB35103 standard; protein; 120 AA.  
DE Human PRO polypeptide SEQ ID NO 434.  
PN US2003077718-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 856  
ID ADB36207 standard; protein; 120 AA.  
DE Human PRO polypeptide SEQ ID NO 434.  
PN US2003077720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 857  
ID ADB46602 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 858  
ID ADC57679 standard; protein; 120 AA.  
DE Human PRO polypeptide #50.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 859  
ID ADC55043 standard; protein; 120 AA.  
DE Human PRO polypeptide #50.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 860  
ID ADC11910 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein PRO1056.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 861  
ID ADC56332 standard; protein; 120 AA.  
DE Human PRO polypeptide #50.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 862

ID ADC07387 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein PRO1056.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 863  
ID ADC11377 standard; protein; 120 AA.  
DE Human secreted/transmembrane protein PRO1056.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 864  
ID ADC50475 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 865  
ID ADC72022 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 866  
ID ADC60001 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 867  
ID ADC53008 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein Seq ID434.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 868  
ID ADC57362 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein Seq ID434.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 869  
ID ADC60553 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 870  
ID ADC51028 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 871  
ID ADC65555 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 872  
ID ADC54653 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein Seq ID434.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 873  
ID ADC53614 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein Seq ID434.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 874  
ID ADC59137 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein Seq ID434.  
PN US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 875  
ID ADC56015 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein Seq ID434.  
PN US2003087360-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 876  
ID ADC58585 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein Seq ID434.  
PN US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 877  
ID ADC14499 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 878  
ID ADD08031 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003068623-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 879  
ID ADD03259 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003092104-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 880  
ID ADC90251 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;

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Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 881
ID ADC81856 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 882
ID ADC69670 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 883
ID ADC48559 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 884
ID ADD10088 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 885
ID ADD07498 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 886
ID ADD04663 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 887
ID ADC82389 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 888
ID ADC80619 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 889
ID ADD11126 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 890
ID ADC48007 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003203437-A1.
PD 30-OCT-2003.

DE Human PRO polypeptide #217.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 891
ID ADD08569 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 892
ID ADC80067 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 893
ID ADD06818 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 894
ID ADD09536 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 895
ID ADC83065 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 896
ID ADD41249 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 897
ID ADD52388 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 898
ID ADD53128 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 899
ID ADD53680 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003203437-A1.
PD 30-OCT-2003.
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PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 900  
ID ADD55172 standard; protein; 120 AA.  
DE Human PRO polypeptide #50.  
PN US2003077593-A1.  
PD 24-APR-2003.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 901  
ID ADD56130 standard; protein; 120 AA.  
DE Human PRO polypeptide #50.  
PN US2003077594-A1.  
PD 24-APR-2003.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 902  
ID ADD51836 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 903  
ID ADD02635 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US20031203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 904  
ID ADD02069 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 905  
ID ADD54251 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 906  
ID ADD54568 standard; protein; 120 AA.  
DE Human PRO polypeptide #50.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 907  
ID ADD92568 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003199030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 908  
ID ADD91464 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003199055-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 909  
ID ADE04078 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003199057-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 910  
ID ADE26722 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 911  
ID ADE32375 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 912  
ID ADE22307 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 913  
ID ADD79531 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 914  
ID ABE42067 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 915  
ID ADE17884 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003199023-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 916  
ID ADD92016 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003199053-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 917  
ID ADE33479 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003194767-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 918  
ID ADE34031 standard; protein; 120 AA.

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DE Novel human secreted and transmembrane protein PRO1056.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 24.4%; Score 112.5; DB 7; Length 120;
RESULT 919
ID ADE80083 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 24.4%; Score 112.5; DB 7; Length 120;
RESULT 920
ID ADE42619 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 24.4%; Score 112.5; DB 7; Length 120;
RESULT 921
ID ADE19540 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 24.4%; Score 112.5; DB 7; Length 120;
RESULT 922
ID ADE19888 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 24.4%; Score 112.5; DB 7; Length 120;
RESULT 923
ID ADE43184 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 24.4%; Score 112.5; DB 7; Length 120;
RESULT 924
ID ADD95973 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 24.4%; Score 112.5; DB 7; Length 120;
RESULT 925
ID ADE22859 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 24.4%; Score 112.5; DB 7; Length 120;
RESULT 926
ID ADD78977 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 24.4%; Score 112.5; DB 7; Length 120;
RESULT 927
ID ADE26189 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 24.4%; Score 112.5; DB 7; Length 120;
RESULT 928
ID ADE32927 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 24.4%; Score 112.5; DB 7; Length 120;
RESULT 929
ID ADE42619 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 24.4%; Score 112.5; DB 7; Length 120;
RESULT 930
ID ADD80635 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 24.4%; Score 112.5; DB 7; Length 120;
RESULT 931
ID ADD89663 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 24.4%; Score 112.5; DB 7; Length 120;
RESULT 932
ID ADE40947 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 24.4%; Score 112.5; DB 7; Length 120;
RESULT 933
ID ADE04746 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 24.4%; Score 112.5; DB 7; Length 120;
RESULT 934
ID ADE92875 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 24.4%; Score 112.5; DB 7; Length 120;
RESULT 935
ID ADF67126 standard; protein; 120 AA.
DE Human PRO1056 amino acid sequence SEQ ID NO:199.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 24.4%; Score 112.5; DB 7; Length 120;
RESULT 936
ID ADE21584 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207355-A1.
PD 06-NOV-2003.
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Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 946  
ID ADI63583 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207387-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 947  
ID ADH81997 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207388-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 948  
ID ADH99872 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 949  
ID ADH81445 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 950  
ID ADM82614 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 951  
ID ADN16013 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 952  
ID ADN16642 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 953  
ID ADN15461 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 954  
ID ADN14909 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 955  
ID ADN14909 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 7; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;



ID ADC81171 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 956  
ID ADD76619 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 957  
ID ADD87983 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 958  
ID ADD86387 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 959  
ID ADE75835 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 960  
ID ADE23411 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003092108-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 961  
ID ADE23963 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003092110-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 962  
ID ADE24606 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003092111-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 963  
ID ADD87431 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003203439-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 964  
ID ADE89297 standard; protein; 120 AA.

DE Human PRO polypeptide #217.  
PN US2003199062-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 965  
ID ADE18436 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003194794-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 966  
ID ADE89745 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003199054-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 967  
ID ADE94765 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003199027-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 968  
ID ADS91176 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003199061-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 969  
ID ADF35325 standard; protein; 120 AA.  
DE Human PRO1056 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 970  
ID ADE95317 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003199052-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 971  
ID ADE93427 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003199060-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 972  
ID ADF35008 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003199029-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 973  
ID ADE92323 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003199051-A1.

PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 974  
ID ADE90624 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US200319063-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 975  
ID ADE91771 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 976  
ID ADG11575 standard; protein; 120 AA.  
DE Human PRO1056 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 977  
ID ADG02350 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 978  
ID ADG22136 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 979  
ID ADG20206 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 980  
ID ADF98112 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 981  
ID ADG24329 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 982  
ID ADF98683 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003208055-A1.  
PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 983  
ID ADG03514 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003207351-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 984  
ID ADF99235 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003207353-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 985  
ID ADG16820 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 986  
ID ADG05279 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003207375-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 987  
ID ADG19546 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003207425-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 988  
ID ADG13383 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003207357-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 989  
ID ADG08440 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207424-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 990  
ID ADG15610 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003219885-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 991  
ID ADF97008 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003207371-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.

Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 992  
ID ADG06193 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003207374-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 993  
ID ADG233777 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207389-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 994  
ID ADG04066 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003207423-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 995  
ID ADG24967 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207427-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 996  
ID ADG07264 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207350-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 997  
ID ADG07816 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207356-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 998  
ID ADG55311 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003194778-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 999  
ID ADG60975 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 1000  
ID ADG62079 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207428-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;

Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 1001  
ID ADG82280 standard; protein; 120 AA.  
DE Human PRO polypeptide #217.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 1002  
ID ADG57519 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 1003  
ID ADG56967 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 1004  
ID ADG55863 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 1005  
ID ADG58623 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 1006  
ID ADG70989 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 1007  
ID ADG58071 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 1008  
ID ADG53655 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;  
RESULT 1009  
ID ADG71541 standard; protein; 120 AA.  
DE Novel human secreted and transmembrane protein PRO1056.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 24.4%; Score 112.5; DB 8; Length 120;  
Best Local Similarity 36.0%; Pred. No. 9e-06;

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RESULT 1010
ID ADG81728 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1011
ID ADG19445 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1012
ID ADH30690 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1013
ID ADH12057 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1014
ID ADG52479 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1015
ID ADG54207 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1016
ID ADG81176 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1017
ID ADG56415 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1018
ID ADH12681 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1019
ID ADH20938 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2004009547-A1.
DE Human secreted/transmembrane protein PRO1056.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1020
ID ADG61527 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207429-A1.
PD 08-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1021
ID ADH19978 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1022
ID ADH28614 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1023
ID ADG54759 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1024
ID ADG59799 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1025
ID ADI81223 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1026
ID ADG09966 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1027
ID ADI15437 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1028
ID ADG09314 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2004009547-A1.
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PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1029
ID AD114769 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1030
ID AD118364 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1031
ID ADJ3645 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1032
ID ADJ7540 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1033
ID ADJ5662 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1034
ID ADM27798 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1035
ID ADM4252 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1036
ID ADM28384 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1037
ID ADI95866 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1038
ID ADI96418 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1039
ID ADS32370 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1040
ID ADT03354 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1041
ID ADZ03405 standard; protein; 120 AA.
DE Human secreted/transmembrane PRO1056 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 9; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1042
ID AEA38462 standard; protein; 120 AA.
DE Human secreted/transmembrane protein, #118.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 9; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1043
ID AEB14151 standard; protein; 120 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 434.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE//) BAKER K P.
PA (BERE//) BERESINI M.
PA (DEFO//) DEFORGE L.
PA (DESN//) DESNOYERS L.
PA (FILV//) FILVAROFF E.
PA (GAOW//) GAO W.
PA (GERR//) GERRITSEN M E.
PA (GODD//) GODDARD A.
PA (GODO//) GODORSKI P J.
PA (GURN//) GURNEY A L.
PA (SHER//) SHERWOOD S.
PA (SMIT//) SMITH V.
PA (STEW//) STEWART T A.
PA (TUMA//) TUMAS D.
PA (WATA//) WATANABE C K.
PA (WOOD//) WOOD W I.
PA (ZHAN//) ZHANG Z.
Query Match 24.4%; Score 112.5; DB 9; Length 120;
Best Local Similarity 36.0%; Pred. No. 9e-06;
RESULT 1044
ID ABB80585 standard; protein; 95 AA.
DE Human sbg1015258PLM protein.
PN WO200222802-A1.
PD 21-MAR-2002.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
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PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PA (GLAX ) GLAXO GROUP LTD.  
Query Match 24.3%; Score 112; DB 5; Length 95;  
Best Local Similarity 35.9%; Pred. No. 7.7e-06;  
RESULT 1045  
ID AAW75005 standard; protein; 69 AA.  
DE Human secreted protein encoded by gene 154 clone HB6FL83.  
PN WO9839448-A2.  
PD 11-SEP-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 23.0%; Score 106; DB 2; Length 69;  
Best Local Similarity 40.0%; Pred. No. 2.9e-05;  
RESULT 1046  
ID ABG95466 standard; protein; 69 AA.  
DE Human novel secreted protein #287.  
PN US6420526-B1.  
PD 16-JUL-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 23.0%; Score 106; DB 5; Length 69;  
Best Local Similarity 40.0%; Pred. No. 2.9e-05;  
RESULT 1047  
ID AB034660 standard; protein; 69 AA.  
DE Region of human secreted protein encoded by cDNA sequence #287.  
PN US2003049618-A1.  
PD 13-MAR-2003.  
PA (RUBE/) RUBEN S M.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (CART/) CARTER K C.  
PA (BEDN/) BEDNARIK D P.  
PA (ENDR/) ENDRESS G A.  
PA (YUGG/) YU G.  
PA (NIJJ/) NI J.  
PA (FENG/) FENG P.  
PA (YOUN/) YOUNG P E.  
PA (GREE/) GREENE J M.  
PA (FERR/) FERRIE A M.  
PA (DUAN/) DUAN D R.  
PA (HUJJ/) HU J.  
PA (FLOR/) FLORENCE K A.  
PA (OLSE/) OLSEN H S.  
PA (FISC/) FISCHER C L.  
PA (EBNE/) EBER R.  
PA (BREW/) BREWER L A.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (LAFLE/) LAFLEUR D W.  
PA (LIYV/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (KYAW/) KYAW H.  
Query Match 23.0%; Score 106; DB 6; Length 69;  
Best Local Similarity 40.0%; Pred. No. 2.9e-05;  
RESULT 1048  
ID AD123321 standard; protein; 69 AA.  
DE Novel human secreted protein seq id 606.  
PN US2003175858-A1.  
PD 18-SEP-2003.  
PA (RUBE/) RUBEN S M.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (CART/) CARTER K C.  
PA (BEDN/) BEDNARIK D P.  
PA (ENDR/) ENDRESS G A.  
PA (YUGG/) YU G.  
PA (NIJJ/) NI J.  
PA (FENG/) FENG P.  
PA (YOUN/) YOUNG P E.  
PA (GREE/) GREENE J M.  
PA (FERR/) FERRIE A M.  
PA (DUAN/) DUAN D R.  
PA (HUJJ/) HU J.  
PA (FLOR/) FLORENCE K A.  
PA (OLSE/) OLSEN H S.

PA (FISC/) FISCHER C L.  
PA (EBNE/) EBER R.  
PA (BREW/) BREWER L A.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (LAFLE/) LAFLEUR D W.  
PA (LIYV/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (KYAW/) KYAW H.  
Query Match 23.0%; Score 106; DB 7; Length 69;  
Best Local Similarity 40.0%; Pred. No. 2.9e-05;  
RESULT 1049  
ID ADH74323 standard; protein; 69 AA.  
DE Human secreted protein #287.  
PN US2003225248-A1.  
PD 04-DEC-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 23.0%; Score 106; DB 8; Length 69;  
Best Local Similarity 40.0%; Pred. No. 2.9e-05;  
RESULT 1050  
ID ABG26346 standard; protein; 110 AA.  
DE Novel human diagnostic protein #26337.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 22.9%; Score 105.5; DB 4; Length 110;  
Best Local Similarity 33.8%; Pred. No. 6.2e-05;  
RESULT 1051  
ID AAY13121 standard; protein; 72 AA.  
DE Human secreted protein encoded by 5' EST SEQ ID NO: 135.  
PN WO9906552-A2.  
PD 11-FEB-1999.  
PA (GBST ) GENSET.  
Query Match 21.6%; Score 99.5; DB 2; Length 72;  
Best Local Similarity 36.4%; Pred. No. 0.00021;  
RESULT 1052  
ID ABP03457 standard; protein; 63 AA.  
DE Human ORFX protein sequence SEQ ID NO:6896.  
PN WO200192523-A2.  
PD 06-DEC-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 20.8%; Score 96; DB 5; Length 63;  
Best Local Similarity 32.8%; Pred. No. 0.00048;  
RESULT 1053  
ID ABG75825 standard; protein; 80 AA.  
DE Transporters and ion channels protein 7, TRICH-7.  
PN WO2003016493-A2.  
PD 27-FEB-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 20.6%; Score 95; DB 6; Length 80;  
Best Local Similarity 31.3%; Pred. No. 0.00088;  
RESULT 1054  
ID ABM85184 standard; protein; 148 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5433.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 20.6%; Score 95; DB 8; Length 148;  
Best Local Similarity 36.5%; Pred. No. 0.0019;  
RESULT 1055  
ID ABR82718 standard; protein; 115 AA.  
DE Human IWU-1 protein.  
PN WO2003064603-A2.  
PD 07-AUG-2003.  
PA (UTRP ) UNIV ROCHESTER.  
Query Match 20.4%; Score 94; DB 7; Length 115;  
Best Local Similarity 43.9%; Pred. No. 0.0019;  
RESULT 1056  
ID ABM85185 standard; protein; 147 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5434.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.

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Query Match
Best Local Similarity 20.4%; Score 94; DB 8; Length 147;
RESULT 1057
ID AAY13945 standard; protein; 178 AA.
DE Human transmembrane protein, HP10479.
PD 15-APR-1999.
PA (SAGA ) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 2; Length 178;
RESULT 1058
ID AAY41674 standard; protein; 178 AA.
DE Human channel-related molecule HCMR-2.
PD 02-SEP-1999.
PA (INCY-) INCYTE PHARM INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 2; Length 178;
RESULT 1059
ID AAU29294 standard; protein; 178 AA.
DE Human PRO polypeptide sequence #271.
PD 20-SEP-2001.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 4; Length 178;
RESULT 1060
ID AAM38819 standard; protein; 178 AA.
DE Human polypeptide SEQ ID NO 1964.
PD W020015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 4; Length 178;
RESULT 1061
ID ASB90357 standard; protein; 178 AA.
DE Human polypeptide SEQ ID NO 2733.
PD W0200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 5; Length 178;
RESULT 1062
ID AAO17172 standard; protein; 178 AA.
DE Human secreted protein SEQ ID NO: 71.
PD W0200228877-A1.
PD 11-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 5; Length 178;
RESULT 1063
ID ABG64783 standard; protein; 178 AA.
DE Human albumin fusion protein #1458.
PD W0200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 5; Length 178;
RESULT 1064
ID ABUS8670 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PD US2003027272-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;
RESULT 1065
ID ABU88218 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PD US2003032127-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;
RESULT 1066
ID ASU84533 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PD US2003032112-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;
RESULT 1067
ID ABR66407 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PD US2003027278-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;
RESULT 1068
ID ABR65797 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PD US2003036159-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;
RESULT 1069
ID ABU99737 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PD US2003040070-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;
RESULT 1070
ID ABU82976 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PD US2003032113-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;
RESULT 1071
ID ABU90097 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PD US2003036147-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;
RESULT 1072
ID ABR68346 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PD US2003027264-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;
RESULT 1073
ID ABU96399 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PD US2003036144-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;
RESULT 1074
ID ABU92830 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PD US2003036149-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;
RESULT 1075
ID ABO08907 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PD US2003044923-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 20.4%; Score 94; DB 6; Length 178;
RESULT 1076
ID ABO02959 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
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PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1077  
ID ABR75113 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1078  
ID ABR94875 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1079  
ID ABUS85848 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1080  
ID ABUS99008 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1081  
ID ABUS98223 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1082  
ID ABUS91929 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1083  
ID ABUS96222 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1084  
ID ABUS86463 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1085  
ID ABUS67676 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1086  
ID ABUS0704 standard; protein; 178 AA.  
DE Human PRO protein #271.

PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1087  
ID ABR99622 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1088  
ID ABR99012 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1089  
ID ABO16535 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1090  
ID ABR92435 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1091  
ID ABO19076 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1092  
ID ABR78497 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1093  
ID ABUS85233 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1094  
ID ABO003172 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1095  
ID ABO11704 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1096  
ID ABO02349 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003040054-A1.



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PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1097
ID ADA41202 standard; protein; 178 AA.
DE Human secreted protein.
PN W02002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1098
ID ABU8923 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1099
ID ABU83618 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1100
ID ABO06419 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1101
ID ABR59455 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1102
ID ABO09517 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1103
ID ABO19381 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1104
ID ABO11399 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1105
ID ABR67017 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1106
ID ABO16230 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1107
ID ABO13936 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1108
ID ABU65839 standard; protein; 178 AA.
DE Human secreted/transmembrane protein, SEQ ID 542.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1109
ID ABO07687 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1110
ID ABO03874 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1111
ID ABR67322 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1112
ID ABO15925 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1113
ID ABU56206 standard; protein; 178 AA.
DE Human secreted/transmembrane protein, PRO6241.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1114
ID ABU65534 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1115
ID ABU95479 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1116
ID ABU71382 standard; protein; 178 AA.
DE Human PRO6241 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
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RESULT 1117
ID ABO07992 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1118
ID ABR70233 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1119
ID ABR69566 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1120
ID ABO01707 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1121
ID ABR81509 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1122
ID ABR60306 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1123
ID ABR68041 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1124
ID ABR65429 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1125
ID ABR68651 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027274-A1.
PD 08-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1126
ID ABR72063 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1127
ID ABR85543 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1128
ID ABR89233 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1129
ID ABR83313 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1130
ID ABR95169 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1131
ID ABR90717 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1132
ID ABR84228 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1133
ID ABR93879 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1134
ID ABR65124 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1135
ID ABR68956 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1136
ID ABO06772 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1137
ID ABR99317 standard; protein; 178 AA.
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[illegible]

RESULT 1158  
ID ABU98703 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1159  
ID ABR66102 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1160  
ID ABR64819 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1161  
ID ABU79744 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1162  
ID ABU93135 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1163  
ID ABU96094 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1164  
ID ABU91314 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1165  
ID ABU90407 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1166  
ID ABO09822 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1167  
ID ABO11094 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1168  
ID ABR71148 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003032115-A1.

DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1169  
ID ABU87756 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1170  
ID ABU91624 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1171  
ID ABU84838 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1172  
ID ABR69928 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1173  
ID ABU80305 standard; protein; 178 AA.  
DE Human PRO protein #271.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1174  
ID ABU93574 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1175  
ID ABO10127 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1176  
ID ABO09212 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1177  
ID ABU10780 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein #271.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1178  
ID ABU95789 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003032115-A1.

PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1179  
ID ABR96998 standard; protein; 178 AA.  
DE Human secreted and transmembrane protein PRO6241.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1180  
ID ABR70843 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1181  
ID ABO05194 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1182  
ID ABO08602 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003044522-A1.  
PD 06-MAR-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1183  
ID ABO05809 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1184  
ID ABR74198 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1185  
ID ABR95790 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1186  
ID ABR81087 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1187  
ID ABR81392 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1188  
ID ABR01088 standard; protein; 178 AA.

DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1189  
ID ABR88690 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1190  
ID ABR77511 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1191  
ID ABO28995 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1192  
ID ABO31740 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1193  
ID ABO08157 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1194  
ID ABO40637 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1195  
ID ABO36062 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1196  
ID ABO44201 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1197  
ID ADA78294 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.

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PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      20.4%; Score 94; DB 6; Length 178;
  Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1198
ID ABR24996 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104539-A1.
PD 03-JUN-2003.
  Query Match      20.4%; Score 94; DB 6; Length 178;
  Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1199
ID ABO03264 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036131-A1.
PD 20-FEB-2003.
  Query Match      20.4%; Score 94; DB 6; Length 178;
  Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1200
ID ABR90520 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040075-A1.
PD 27-FEB-2003.
  Query Match      20.4%; Score 94; DB 6; Length 178;
  Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1201
ID ABR17434 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      20.4%; Score 94; DB 6; Length 178;
  Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1202
ID ABR95180 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003044930-A1.
PD 06-MAR-2003.
  Query Match      20.4%; Score 94; DB 6; Length 178;
  Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1203
ID ABR95485 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match      20.4%; Score 94; DB 6; Length 178;
  Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1204
ID ABO21723 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      20.4%; Score 94; DB 6; Length 178;
  Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1205
ID ABR97987 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      20.4%; Score 94; DB 6; Length 178;
  Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1206
ID ABR87775 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      20.4%; Score 94; DB 6; Length 178;
  Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1207
ID ABR77816 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      20.4%; Score 94; DB 6; Length 178;
  Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1208
ID ABR28046 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064440-A1.
PD 03-APR-2003.
  Query Match      20.4%; Score 94; DB 6; Length 178;
  Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1209
ID ABR06327 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      20.4%; Score 94; DB 6; Length 178;
  Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1210
ID ABR03833 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      20.4%; Score 94; DB 6; Length 178;
  Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1211
ID ABR35284 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      20.4%; Score 94; DB 6; Length 178;
  Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1212
ID ABR28521 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match      20.4%; Score 94; DB 6; Length 178;
  Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1213
ID ABO48303 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      20.4%; Score 94; DB 6; Length 178;
  Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1214
ID ABR93045 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003084462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      20.4%; Score 94; DB 6; Length 178;
  Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1215
ID ABO24806 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      20.4%; Score 94; DB 6; Length 178;
  Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1216
ID ABR11817 standard; protein; 178 AA.
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DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1217  
ID ABO43896 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1218  
ID ABO43896 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1219  
ID ABO27775 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1220  
ID ABO29266 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1221  
ID ABO7242 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1222  
ID ABO21336 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1223  
ID ABO09682 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1224  
ID ABO41552 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1225  
ID ABO36367 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.

PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1226  
ID ABO43896 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1227  
ID ABO76596 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1228  
ID ABO76292 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1229  
ID ABO25911 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1230  
ID ABO26216 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1231  
ID ABO03569 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1232  
ID ABO02654 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1233  
ID ABO90825 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1234  
ID ABO73893 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1235  
ID ABO17145 standard; protein; 178 AA.

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DE Human secreted/transmembrane protein (PRO) #271.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1236
ID ABR94570 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1237
ID ABR76077 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1238
ID ABR71453 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1239
ID ABR93350 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1240
ID ABR93655 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1241
ID ABR88080 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1242
ID ABO28080 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1243
ID ABO30215 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1244
ID ABO33424 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1245
ID ABO5112 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1246
ID ABO5072 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1247
ID ABO36672 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1248
ID ABO35757 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1249
ID ABO39722 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1250
ID ABO10597 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003059407-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1251
ID ABO12122 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1252
ID ABO52268 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1253
ID ABO52573 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
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Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1254  
 ID ABO23891 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003032134-A1.  
 PD 13-FEB-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1255  
 ID ABR97377 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003054481-A1.  
 PD 20-MAR-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1256  
 ID ABR87165 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003049778-A1.  
 PD 13-MAR-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1257  
 ID ABM11207 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003049782-A1.  
 PD 13-MAR-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1258  
 ID ABM28351 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003054476-A1.  
 PD 20-MAR-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1259  
 ID ABO32350 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003068733-A1.  
 PD 10-APR-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1260  
 ID ABM15477 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003068692-A1.  
 PD 10-APR-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1261  
 ID ABM06632 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003068709-A1.  
 PD 10-APR-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1262  
 ID ABM04443 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003068716-A1.  
 PD 10-APR-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1263  
 ID ABM18654 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003054480-A1.

RESULT 1263  
 ID ABM2556 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003068740-A1.  
 PD 10-APR-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1264  
 ID ABM07852 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003068751-A1.  
 PD 10-APR-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1265  
 ID ABO40942 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003068684-A1.  
 PD 10-APR-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1266  
 ID ABM35589 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003073179-A1.  
 PD 17-APR-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1267  
 ID ABM33352 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003087374-A1.  
 PD 08-MAY-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1268  
 ID ABO52878 standard; protein; 178 AA.  
 DE Human PRO polypeptide #271.  
 PN US2003049773-A1.  
 PD 13-MAR-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1269  
 ID ABO50438 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003049777-A1.  
 PD 13-MAR-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1270  
 ID ABU99432 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003040055-A1.  
 PD 27-FEB-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1271  
 ID ABO44484 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003036164-A1.  
 PD 20-FEB-2003.  
 Query Match 20.4%; Score 94; DB 6; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1272  
 ID ABM18654 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003054480-A1.

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PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1273
ID ABR97682 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1274
ID ABR80782 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1275
ID ABR01393 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1276
ID ABR88995 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1277
ID ABR13647 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1278
ID ABR21031 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1279
ID ABR042162 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1280
ID ABR042772 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1281
ID ABR10292 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1282
ID ABR038807 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1283
ID ABR33047 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1284
ID ABR22861 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1285
ID ABR75072 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1286
ID ADA80086 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1287
ID ABR96462 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1288
ID ABR02613 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1289
ID ABR86555 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1290
ID ABR86860 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0033;
RESULT 1291
ID ABR16824 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
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PN	US2003064448-A1.	20.4%;	Score 94;	DB 6;	Length 178;
PD	03-APR-2003.	43.9%;	Pred. No. 0.0033;		
PA	(GETH ) GENENTECH INC.				
Query Match	20.4%;	Score 94;	DB 6;	Length 178;	
Best Local Similarity	43.9%;	Pred. No. 0.0033;			
RESULT 1292					
ID	ABM29876 standard; protein; 178 AA.				
DE	Human secreted polypeptide PRO6241, SEQ ID NO:542.				
PN	US2003064456-A1.				
PD	03-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	20.4%;	Score 94;	DB 6;	Length 178;	
Best Local Similarity	43.9%;	Pred. No. 0.0033;			
RESULT 1293					
ID	ABO29300 standard; protein; 178 AA.				
DE	Human secreted/transmembrane protein (PRO) #271.				
PN	US2003068693-A1.				
PD	10-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	20.4%;	Score 94;	DB 6;	Length 178;	
Best Local Similarity	43.9%;	Pred. No. 0.0033;			
RESULT 1294					
ID	ABM24081 standard; protein; 178 AA.				
DE	Human secreted polypeptide PRO6241, SEQ ID NO:542.				
PN	US2003068735-A1.				
PD	10-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	20.4%;	Score 94;	DB 6;	Length 178;	
Best Local Similarity	43.9%;	Pred. No. 0.0033;			
RESULT 1295					
ID	ABM23471 standard; protein; 178 AA.				
DE	Human secreted polypeptide PRO6241, SEQ ID NO:542.				
PN	US2003068753-A1.				
PD	10-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	20.4%;	Score 94;	DB 6;	Length 178;	
Best Local Similarity	43.9%;	Pred. No. 0.0033;			
RESULT 1296					
ID	ABM22251 standard; protein; 178 AA.				
DE	Human secreted polypeptide PRO6241, SEQ ID NO:542.				
PN	US2003068742-A1.				
PD	10-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	20.4%;	Score 94;	DB 6;	Length 178;	
Best Local Similarity	43.9%;	Pred. No. 0.0033;			
RESULT 1297					
ID	ABO37892 standard; protein; 178 AA.				
DE	Human secreted/transmembrane protein (PRO) #271.				
PN	US2003068756-A1.				
PD	10-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	20.4%;	Score 94;	DB 6;	Length 178;	
Best Local Similarity	43.9%;	Pred. No. 0.0033;			
RESULT 1298					
ID	ABM28656 standard; protein; 178 AA.				
DE	Human secreted polypeptide PRO6241, SEQ ID NO:542.				
PN	US2003082715-A1.				
PD	01-MAY-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	20.4%;	Score 94;	DB 6;	Length 178;	
Best Local Similarity	43.9%;	Pred. No. 0.0033;			
RESULT 1299					
ID	ABM28961 standard; protein; 178 AA.				
DE	Human secreted polypeptide PRO6241, SEQ ID NO:542.				
PN	US2003082716-A1.				
PD	01-MAY-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	20.4%;	Score 94;	DB 6;	Length 178;	
Best Local Similarity	43.9%;	Pred. No. 0.0033;			
RESULT 1300					
ID	ABM66605 standard; protein; 178 AA.				
DE	Human secreted polypeptide PRO6241, SEQ ID NO:542.				
PN	US2003068737-A1.				
PD	10-APR-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	20.4%;	Score 94;	DB 6;	Length 178;	
Best Local Similarity	43.9%;	Pred. No. 0.0033;			
RESULT 1301					
ID	ABM75987 standard; protein; 178 AA.				
DE	Human secreted polypeptide PRO6241, SEQ ID NO:542.				
PN	US2003104547-A1.				
PD	05-JUN-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match	20.4%;	Score 94;	DB 6;	Length 178;	
Best Local Similarity	43.9%;	Pred. No. 0.0033;			
RESULT 1302					
ID	ABM34567 standard; protein; 178 AA.				
DE	Human secret				

ID ABO00783 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1311  
ID ABO00478 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1312  
ID ABO29910 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1313  
ID ABO23776 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1314  
ID ABO29571 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1315  
ID ABO38502 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1316  
ID ABO45802 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1317  
ID ABO20726 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1318  
ID ABO4813 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1319  
ID ABO16840 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003027276-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1320  
ID ABO18466 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1321  
ID ABO22893 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1322  
ID ABO23198 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1323  
ID ABR92740 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1324  
ID ABR81697 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1325  
ID ABO78121 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1326  
ID ABR89910 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003073171-A1.  
PD 17-APR-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1327  
ID ABO28626 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1328  
ID ABO13952 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1329  
ID ABO28690 standard; protein; 178 AA.

DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003064460-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1330  
ID ABO30520 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1331  
ID ABO07547 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1332  
ID ABO04138 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1333  
ID ABO37282 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1334  
ID ABO41857 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1335  
ID ABO35452 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1336  
ID ABM25301 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1337  
ID ABO47693 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1338  
ID ABO47998 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003049747-A1.

PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1339  
ID ABO48608 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1340  
ID ABO51658 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1341  
ID ABO51963 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1342  
ID ABO50743 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1343  
ID ABR79867 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1344  
ID ABM17129 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1345  
ID ABO18161 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1346  
ID ABO21113 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1347  
ID ABR37072 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1348  
ID ABM12427 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1349  
ID ABM16519 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1350  
ID ABM24386 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003064441-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1351  
ID ABM14867 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1352  
ID ABM04748 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1353  
ID ABM06937 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1354  
ID ABM039417 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003073174-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1355  
ID AB039417 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1356  
ID ABM75882 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1357  
ID ABM25606 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.

PN US2003104541-A1.  
PD 05-JUN-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1358  
ID ABW20116 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1359  
ID ABO47022 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1360  
ID ABO47327 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1361  
ID ADA83611 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1362  
ID ABR71758 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1363  
ID ABR72368 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1364  
ID ABR98707 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1365  
ID ABO07077 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1366  
ID ABR85030 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1367  
ID ABR73588 standard; protein; 178 AA.

Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1377  
ID ABO33119 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1378  
ID ABO30825 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1379  
ID ABO31130 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1380  
ID ABM27436 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1381  
ID ABM30181 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1382  
ID ABM05717 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1383  
ID ABM15782 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1384  
ID ABM08767 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1385  
ID AB042467 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1386  
ID ABO38197 standard; protein: 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1387  
ID ABO46107 standard; protein: 178 AA.  
DE Human PRO polypeptide #271.  
FN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1388  
ID ABM66910 standard; protein: 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1389  
ID AD20654 standard; protein: 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1390  
ID ABM19811 standard; protein: 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1391  
ID ABO49523 standard; protein: 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1392  
ID ABO49828 standard; protein: 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1393  
ID ADA78906 standard; protein: 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1394  
ID ABR88385 standard; protein: 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1395  
ID ABM27131 standard; protein: 178 AA.

DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1396  
ID ABM03528 standard; protein: 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1397  
ID ABO40027 standard; protein: 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 6; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1398  
ID ABO50133 standard; protein: 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1399  
ID ABO51048 standard; protein: 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1400  
ID ABO05504 standard; protein: 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003036126-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1401  
ID ABR74808 standard; protein: 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003044924-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1402  
ID ABR77287 standard; protein: 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003044927-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1403  
ID ABM18044 standard; protein: 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003040072-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1404  
ID ABR96095 standard; protein: 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003040073-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;



RESULT 1405  
ID ABO22028 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1406  
ID ABO20198 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003032124-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1407  
ID ABO24501 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1408  
ID ABR86250 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1409  
ID ABM10902 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1410  
ID ABM76901 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1411  
ID ABR89605 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003073170-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1412  
ID ABM12732 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1413  
ID ABM06022 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1414  
ID ABO35147 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
FN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1415  
ID ABM03223 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1416  
ID ABM19201 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1417  
ID ABM19506 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1418  
ID ABO46717 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
FN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1419  
ID ABO49218 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1420  
ID ABR69261 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003027273-A1.  
PD 06-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1421  
ID ABR89300 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003036119-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1422  
ID ABR72673 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003036120-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1423  
ID ABR74503 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;

Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1424  
ID ABO18771 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003044921-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1425  
ID ABR80477 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1426  
ID ABO1698 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1427  
ID ABO2308 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1428  
ID ABR87470 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1429  
ID ABR13037 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1430  
ID ABR30791 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1431  
ID ABR24691 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1432  
ID ABO29605 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1433  
ID ABO31435 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1434  
ID ABR14562 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003068886-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1435  
ID ABR09987 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1436  
ID ABO39112 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1437  
ID ABR34877 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003104538-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1438  
ID ABO51353 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1439  
ID ABO04179 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003036158-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1440  
ID ABO10649 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
FN US2003036151-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1441  
ID ABR77892 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003040067-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1442  
ID ABR79102 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003054456-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1443

Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1443  
 ID ABO24196 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003054482-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1444  
 ID ABR93960 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003054457-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1445  
 ID ABO2003 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003059883-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1446  
 ID ABR78426 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003049764-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1447  
 ID ABR90215 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003073177-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1448  
 ID ABR27741 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003064442-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1449  
 ID ABR13342 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003064450-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1450  
 ID ABO32045 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003068731-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1451  
 ID ABR14257 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003068683-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1452  
 ID ABR08462 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003068754-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1453  
 ID ABO40332 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003068681-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1454  
 ID ABR74767 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003096351-A1.  
 PD 22-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1455  
 ID ABR33962 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003096358-A1.  
 PD 22-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1456  
 ID ABR20421 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003104556-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1457  
 ID ABO48913 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003049756-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1458  
 ID ABR72978 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003036122-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1459  
 ID ABO15620 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003036121-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1460  
 ID ABR85335 standard; protein; 178 AA.  
 DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
 PN US2003040065-A1.  
 PD 27-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 20.4%; Score 94; DB 7; Length 178;  
 Best Local Similarity 43.9%; Pred. No. 0.0033;  
 RESULT 1461  
 ID ABO15315 standard; protein; 178 AA.  
 DE Human secreted/transmembrane protein (PRO) #271.  
 PN US2003044919-A1.  
 PD 06-MAR-2003.

ID ABM15172 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Similarity 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1472  
ID AB041247 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Similarity 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1473  
ID AB036977 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Similarity 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1474  
ID AB037587 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Similarity 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1475  
ID ABM75377 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Similarity 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1476  
ID ABM33657 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
FN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Similarity 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1477  
ID ABO46412 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
FN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Similarity 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1478  
ID ADA82977 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
FN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match Similarity 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1479  
ID AOB91706 standard; protein; 178 AA.  
DE Human secreted protein #SEQ ID 652.  
FN WO2003004622-A2.  
PD 16-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match Similarity 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1480  
ID ABM32011 standard; protein; 178 AA.

DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068680-A1.  
PD 10-APR-2003.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1481  
ID AEM31401 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1482  
ID ADB86285 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1483  
ID AEM32316 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1484  
ID AEM32621 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1485  
ID AEM31706 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1486  
ID AEM31096 standard; protein; 178 AA.  
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1487  
ID ADD06015 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1488  
ID ADG03010 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1489  
ID ADG01717 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003207399-A1.

PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1490  
ID ADF95892 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1491  
ID ADF74108 standard; protein; 178 AA.  
DE Human cell adhesion inhibitor protein disadherin.  
PN JP2003174885-A.  
PD 24-JUN-2003.  
PA (KOKU-) KOKURITSU GAN CENT SOCHO.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1492  
ID ADG12707 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003207392-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1493  
ID ADH09367 standard; protein; 178 AA.  
DE Human PRO polypeptide #271.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1494  
ID ADL33146 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1495  
ID ADM30682 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1496  
ID ADP65271 standard; protein; 178 AA.  
DE Human FXD domain-containing ion transport regulator 5, dysadherin.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 20.4%; Score 94; DB 7; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1497  
ID ADE74679 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 8; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1498  
ID ADE75291 standard; protein; 178 AA.  
DE Human secreted/transmembrane protein (PRO) #271.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 8; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;

RESULT 1499  
ID ADF96504 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
Query Match 20.4%; Score 94; DB 8; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;  
RESULT 1500  
ID ADG04775 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein PRO6241.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 20.4%; Score 94; DB 8; Length 178;  
Best Local Similarity 43.9%; Pred. No. 0.0033;

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OM protein - protein search, using sw model

Run on: May 12, 2006, 21:28:50 ; Search time 47 Seconds  
(without alignments)  
156.556 Million cell updates/sec

Title: US-10-063-557-50

Perfect score: 461

Sequence: 1 MERVTLALLLAGLTALEAN.....HSPVPEKAIPITPGSATTC 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1500 summaries

#### Database :

Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5 COMB.pep:\*

2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/H-COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/PCRTUS COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/RE COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	461	100.0	89	2	US-09-289-349-11
2	461	100.0	89	2	US-09-991-181-262
3	461	100.0	89	2	US-09-990-444-262
4	461	100.0	89	2	US-09-997-333-262
5	461	100.0	89	2	US-09-992-598-262
6	276.5	60.0	88	2	US-09-724-864-58
7	256.5	55.6	87	1	US-08-725-531-5
8	256.5	55.6	87	1	US-08-738-127-5
9	256.5	55.6	87	1	US-09-213-392-5
10	256.5	55.6	87	1	US-09-083-661-5
11	214.5	46.5	87	1	US-08-289-247B-4
12	214.5	46.5	87	1	US-08-725-531-4
13	214.5	46.5	87	1	US-08-738-127-4
14	214.5	46.5	87	1	US-09-213-392-4
15	214.5	46.5	87	1	US-09-083-661-4
16	214.5	46.5	124	2	US-09-949-016-8238
17	214.5	46.5	124	2	US-09-949-016-8239
18	191.5	41.5	178	2	US-09-949-016-9028
19	191.5	41.5	178	2	US-09-949-016-9029
20	131	28.4	106	2	US-09-621-976-5338
21	131	28.4	107	2	US-09-621-976-5332
22	129	28.0	92	1	US-08-738-127-1
23	129	28.0	92	2	US-08-247-155-120
24	129	28.0	92	2	US-09-148-545-238
25	129	28.0	92	2	US-09-621-011-238
26	129	28.0	92	2	US-09-903-190-120
27	129	28.0	93	2	US-09-148-545-183
28	129	28.0	93	2	US-09-148-545-183
29	126.5	27.4	92	1	US-08-725-531-3
30	126.5	27.4	92	1	US-08-738-127-3
31	126.5	27.4	92	1	US-09-213-392-3
32	126.5	27.4	92	1	US-09-083-661-3
33	121	26.2	70	2	US-09-148-545-269
34	121	26.2	70	2	US-09-621-011-269
35	112.5	24.4	95	1	US-08-725-531-1
36	112.5	24.4	95	1	US-09-213-392-1
37	112.5	24.4	95	1	US-09-083-661-1
38	112.5	24.4	96	2	US-09-149-476-473
39	112.5	24.4	120	2	US-09-991-181-199
40	112.5	24.4	120	2	US-09-990-444-199
41	112.5	24.4	120	2	US-09-997-333-199
42	112.5	24.4	120	2	US-09-992-598-199
43	106	23.0	69	2	US-09-149-476-606
44	103.5	22.5	95	2	US-09-621-976-5250
45	99.5	21.6	72	2	US-08-905-223-405
46	94	20.4	179	2	US-09-205-258-424
47	94	20.4	179	2	US-10-004-860-424
48	89	19.3	80	2	US-09-621-976-6085
49	83	18.0	86	2	US-09-949-016-8419
50	83	18.0	86	2	US-09-949-016-8420
51	73.5	15.9	58	1	US-08-725-531-6
52	73.5	15.9	58	1	US-09-213-392-6
53	73.5	15.9	58	1	US-09-083-661-6
54	73.5	15.9	58	1	US-09-268-140-2
55	67.5	14.6	664	2	US-09-949-016-9005
56	67.5	14.6	664	2	US-09-198-452A-1112
57	66.5	14.4	376	2	US-09-438-185A-1038
58	66.5	14.4	388	2	US-09-949-016-6195
59	66.5	14.4	523	2	US-09-949-016-6195
60	66.5	14.4	552	2	US-09-949-016-8164
61	64.5	14.0	739	2	US-09-248-796A-17121
62	63	13.7	627	2	US-10-222-100-3
63	62.5	13.6	339	2	US-09-690-454-66
64	62.5	13.6	340	2	US-09-690-454-174
65	62.5	13.6	389	2	US-09-328-352-7324
66	62	13.4	78	2	US-09-749-637A-342
67	62	13.4	360	2	US-09-489-039A-8000
68	62	13.4	601	2	US-09-336-443A-4
69	61.5	13.3	103	2	US-09-107-532A-3725
70	61.5	13.3	433	2	US-09-198-452A-925
71	61.5	13.3	453	2	US-09-438-185A-860
72	61.5	13.3	549	2	US-09-120-365-3
73	61.5	13.3	549	2	US-09-515-039-3
74	61.5	13.3	606	2	US-09-270-767-41830
75	61.5	13.3	990	2	US-10-363-337-7
76	61	13.2	457	2	US-09-489-039A-12762
77	60.5	13.1	106	2	US-09-149-476-341
78	60.5	13.1	288	2	US-09-386-642-13
79	60.5	13.1	998	2	US-09-252-991A-28424
80	60	13.0	234	2	US-09-248-796A-17625
81	60	13.0	337	2	US-08-930-830B-2
82	60	13.0	342	2	US-08-930-830B-5
83	60	13.0	404	2	US-09-949-016-7352
84	60	13.0	426	2	US-09-252-991A-27522
85	60	13.0	497	2	US-09-718-693A-1
86	59	12.8	83	2	US-09-227-357-652
87	59	12.8	83	2	US-09-973-278-370
88	59	12.8	430	2	US-09-134-000C-4819
89	59	12.8	539	1	US-08-464-340A-13
90	59	12.8	806	2	US-09-833-466-13
91	59	12.8	854	2	US-09-833-466-12
92	59	12.8	858	2	US-09-275-252A-6
93	58.5	12.7	142	2	US-09-543-681A-5222
94	58.5	12.7	200	2	US-09-252-991A-27855
95	58.5	12.7	243	2	US-09-107-532A-4908
96	58.5	12.7	260	2	US-09-070-526-2
97	58.5	12.7	260	2	US-09-618-259-7
98	58.5	12.7	260	2	US-09-999-833A-395
99	58.5	12.7	260	2	US-10-020-445A-395
100	58.5	12.7	383	1	US-08-314-596-41

Sequence 183, Appli  
Sequence 3, Appli  
Sequence 3, Appli  
Sequence 3, Appli  
Sequence 3, Appli  
Sequence 269, Appl  
Sequence 269, Appl  
Sequence 1, Appli  
Sequence 1, Appli  
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Sequence 473, Appl  
Sequence 199, Appl  
Sequence 199, Appl  
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Sequence 199, Appl  
Sequence 606, Appl  
Sequence 5350, Ap  
Sequence 405, Appl  
Sequence 424, Appl  
Sequence 424, Appl  
Sequence 6085, Ap  
Sequence 8419, Ap  
Sequence 8420, Ap  
Sequence 6, Appli  
Sequence 6, Appli  
Sequence 6, Appli  
Sequence 2, Appli  
Sequence 9005, Ap  
Sequence 1112, Ap  
Sequence 1038, Ap  
Sequence 6195, Ap  
Sequence 8164, Ap  
Sequence 17121, A  
Sequence 3, Appli  
Sequence 66, Appli  
Sequence 174, Appl  
Sequence 7324, Ap  
Sequence 342, Appl  
Sequence 8000, Ap  
Sequence 4, Appli  
Sequence 3725, Ap  
Sequence 825, Appl  
Sequence 960, Appl  
Sequence 3, Appli  
Sequence 3, Appli  
Sequence 41630, A  
Sequence 7, Appli  
Sequence 12762, A  
Sequence 341, Appl  
Sequence 13, Appl  
Sequence 28424, A  
Sequence 17625, A  
Sequence 2, Appli  
Sequence 5, Appli  
Sequence 7352, Ap  
Sequence 27522, A  
Sequence 1, Appli  
Sequence 652, Appl  
Sequence 370, Appl  
Sequence 4819, Ap  
Sequence 13, Appl  
Sequence 13, Appl  
Sequence 12, Appl  
Sequence 6, Appli  
Sequence 5222, Ap  
Sequence 27855, A  
Sequence 4908, Ap  
Sequence 7, Appli  
Sequence 395, Appl  
Sequence 395, Appl  
Sequence 41, Appli

101	58.5	12.7	383	1	US-08-320-982-41	Sequence 41, Appl	174	56.5	12.3	939	2	US-09-520-781-4	Sequence 4, Appl
102	58.5	12.7	383	2	US-08-819-037-41	Sequence 41, Appl	175	56.5	12.3	939	2	US-09-527-187-4	Sequence 4, Appl
103	58.5	12.7	383	2	US-08-530-862B-6	Sequence 6, Appl	176	56.5	12.3	939	2	US-09-951-053-4	Sequence 4, Appl
104	58.5	12.7	383	2	US-08-597-313D-6	Sequence 6, Appl	177	56.5	12.3	1030	2	US-09-856-681A-2	Sequence 2, Appl
105	58.5	12.7	383	2	US-09-059-769-9	Sequence 9, Appl	178	56.5	12.3	1030	2	US-09-856-681A-7	Sequence 7, Appl
106	58.5	12.7	383	2	US-09-161-994A-14	Sequence 14, Appl	179	56.5	12.3	1047	2	US-09-957-187-85	Sequence 85, Appl
107	58.5	12.7	383	2	US-09-133-962A-2	Sequence 2, Appl	180	56	12.1	199	2	US-09-543-681A-5720	Sequence 5720, Ap
108	58.5	12.7	383	2	US-09-045-940-41	Sequence 41, Appl	181	56	12.1	202	2	US-09-489-039A-8619	Sequence 8619, Ap
109	58.5	12.7	383	2	US-08-763-331-4	Sequence 41, Appl	182	56	12.1	316	2	US-09-540-236-3467	Sequence 3467, Ap
110	58.5	12.7	383	2	US-09-697-379-2	Sequence 2, Appl	183	56	12.1	579	2	US-09-540-236-2071	Sequence 2071, Ap
111	58.5	12.7	383	2	US-10-116-212A-2	Sequence 2, Appl	184	56	12.1	593	2	US-09-949-016-10355	Sequence 10355, A
112	58.5	12.7	383	2	US-09-885-189-6	Sequence 6, Appl	185	56	12.1	605	2	US-09-252-991A-24349	Sequence 24349, A
113	58.5	12.7	383	2	US-09-902-540-14949	Sequence 14949, A	186	56	12.1	1058	2	US-09-949-016-11457	Sequence 11457, A
114	58.5	12.7	1058	2	US-09-489-039A-11177	Sequence 11177, A	187	56	12.1	1384	2	US-08-826-134-2	Sequence 2, Appl
115	58	12.6	228	2	US-09-489-039A-10271	Sequence 10271, A	188	56	12.1	1384	2	US-09-949-016-6395	Sequence 6395, Ap
116	58	12.6	427	2	US-09-902-540-14326	Sequence 14326, A	189	56	12.1	1384	2	US-09-902-540-12892	Sequence 12892, A
117	58	12.6	681	2	US-10-104-047-3586	Sequence 3586, Ap	190	56	12.1	1633	2	US-09-949-016-8246	Sequence 8246, Ap
118	57.5	12.5	27	2	US-09-962-756-1644	Sequence 1644, Ap	191	55.5	12.0	175	2	US-09-252-991A-32945	Sequence 32945, A
119	57.5	12.5	352	2	US-09-252-991A-17455	Sequence 17455, A	192	55.5	12.0	248	1	US-08-313-553-3	Sequence 3, Appl
120	57.5	12.5	471	2	US-09-252-991A-27897	Sequence 27897, A	193	55.5	12.0	248	1	US-08-303-651-2	Sequence 2, Appl
121	57.5	12.5	471	2	US-08-328-352-5145	Sequence 5145, Ap	194	55.5	12.0	248	2	US-08-767-993-3	Sequence 3, Appl
122	57.5	12.5	499	2	US-09-902-540-12205	Sequence 12205, A	195	55.5	12.0	262	1	US-08-313-553-2	Sequence 2, Appl
123	57.5	12.5	528	1	US-08-527-152-2	Sequence 2, Appl	196	55.5	12.0	262	2	US-08-767-993-2	Sequence 2, Appl
124	57.5	12.5	775	2	US-09-252-991A-28461	Sequence 28461, A	197	55.5	12.0	292	1	US-08-555-568B-19	Sequence 19, Appl
125	57.5	12.5	1107	2	US-09-489-039A-8890	Sequence 8890, Ap	198	55.5	12.0	292	2	US-09-519-223-19	Sequence 19, Appl
126	57	12.4	185	2	US-10-018-924-6	Sequence 6, Appl	199	55.5	12.0	292	2	US-09-927-180-19	Sequence 19, Appl
127	57	12.4	647	2	US-09-543-681A-5240	Sequence 5240, Ap	200	55.5	12.0	348	2	US-09-248-796A-19460	Sequence 19460, A
128	56.5	12.3	89	1	US-07-939-501A-2	Sequence 2, Appl	201	55.5	12.0	384	1	US-08-675-650B-2	Sequence 2, Appl
129	56.5	12.3	89	1	US-07-966-187-5	Sequence 5, Appl	202	55.5	12.0	384	2	US-09-354-231B-14	Sequence 14, Appl
130	56.5	12.3	89	1	US-08-371-121-4	Sequence 4, Appl	203	55.5	12.0	384	2	US-09-354-231B-16	Sequence 16, Appl
131	56.5	12.3	89	2	US-07-927-391-6	Sequence 6, Appl	204	55.5	12.0	384	2	US-09-354-231B-18	Sequence 18, Appl
132	56.5	12.3	89	2	US-08-115-753-15	Sequence 15, Appl	205	55.5	12.0	384	2	US-09-128-602B-14	Sequence 14, Appl
133	56.5	12.3	158	2	US-09-107-532A-6092	Sequence 6092, Ap	206	55.5	12.0	384	2	US-09-128-602B-16	Sequence 16, Appl
134	56.5	12.3	168	2	US-09-898-659-16	Sequence 16, Appl	207	55.5	12.0	384	2	US-09-128-602B-18	Sequence 18, Appl
135	56.5	12.3	205	2	US-08-818-112-80	Sequence 80, Appl	208	55.5	12.0	384	2	US-09-995-297-14	Sequence 14, Appl
136	56.5	12.3	205	2	US-08-818-111-81	Sequence 81, Appl	209	55.5	12.0	384	2	US-09-995-297-16	Sequence 16, Appl
137	56.5	12.3	205	2	US-09-056-556-80	Sequence 80, Appl	210	55.5	12.0	384	2	US-09-995-297-18	Sequence 18, Appl
138	56.5	12.3	205	2	US-09-072-596-81	Sequence 81, Appl	211	55.5	12.0	391	2	US-09-489-039A-9791	Sequence 9791, Ap
139	56.5	12.3	205	2	US-09-072-967-80	Sequence 80, Appl	212	55.5	12.0	445	4	PCT-US94-05387-7	Sequence 7, Appl
140	56.5	12.3	205	2	US-10-193-002-81	Sequence 81, Appl	213	55.5	12.0	559	1	US-08-313-553-15	Sequence 15, Appl
141	56.5	12.3	205	2	US-10-084-843-80	Sequence 80, Appl	214	55.5	12.0	559	2	US-08-767-993-15	Sequence 15, Appl
142	56.5	12.3	213	2	US-09-605-703B-2594	Sequence 2594, Ap	215	55.5	12.0	687	1	US-08-555-568B-21	Sequence 21, Appl
143	56.5	12.3	233	2	US-08-818-112-76	Sequence 76, Appl	216	55.5	12.0	687	2	US-09-519-223-21	Sequence 21, Appl
144	56.5	12.3	233	2	US-08-818-111-77	Sequence 77, Appl	217	55.5	12.0	687	2	US-09-927-180-21	Sequence 21, Appl
145	56.5	12.3	233	2	US-09-086-556-76	Sequence 76, Appl	218	55.5	12.0	688	1	US-08-555-568B-23	Sequence 23, Appl
146	56.5	12.3	233	2	US-09-072-596-77	Sequence 77, Appl	219	55.5	12.0	688	2	US-09-519-223-23	Sequence 23, Appl
147	56.5	12.3	233	2	US-09-072-967-76	Sequence 76, Appl	220	55.5	12.0	688	2	US-09-927-180-23	Sequence 23, Appl
148	56.5	12.3	233	2	US-10-193-002-77	Sequence 77, Appl	221	55.5	12.0	819	2	US-09-949-016-10948	Sequence 10948, A
149	56.5	12.3	233	2	US-10-084-843-76	Sequence 76, Appl	222	55.5	12.0	887	2	US-09-077-940A-2	Sequence 2, Appl
150	56.5	12.3	260	2	US-09-008-271A-7	Sequence 7, Appl	223	55.5	12.0	888	2	US-09-228-986-76	Sequence 76, Appl
151	56.5	12.3	260	2	US-09-968-415-7	Sequence 7, Appl	224	55.5	12.0	968	2	US-10-101-464A-76	Sequence 76, Appl
152	56.5	12.3	385	1	US-08-416-756A-3	Sequence 3, Appl	225	55.5	12.0	968	2	US-09-270-767-33906	Sequence 33906, A
153	56.5	12.3	385	2	US-08-880-865-3	Sequence 3, Appl	226	55	11.9	124	2	US-09-270-767-49123	Sequence 49123, A
154	56.5	12.3	419	2	US-08-115-753-2	Sequence 2, Appl	227	55	11.9	134	2	US-09-270-767-49123	Sequence 15224, A
155	56.5	12.3	419	2	US-08-115-753-33	Sequence 33, Appl	228	55	11.9	205	2	US-09-248-796A-15224	Sequence 39, Appl
156	56.5	12.3	601	2	US-09-949-016-9977	Sequence 9977, Ap	229	55	11.9	232	1	US-08-456-670B-39	Sequence 39, Appl
157	56.5	12.3	626	2	US-09-957-187-83	Sequence 83, Appl	230	55	11.9	232	2	US-09-372-036-39	Sequence 39, Appl
158	56.5	12.3	630	2	US-09-520-781-30	Sequence 30, Appl	231	55	11.9	359	2	US-09-248-796A-18202	Sequence 18202, A
159	56.5	12.3	630	2	US-09-957-187-30	Sequence 30, Appl	232	55	11.9	376	2	US-09-103-331-47	Sequence 42, Appl
160	56.5	12.3	690	2	US-09-991-053-30	Sequence 30, Appl	233	55	11.9	376	2	US-09-631-594-51	Sequence 51, Appl
161	56.5	12.3	697	2	US-10-101-464A-940	Sequence 940, App	234	55	11.9	381	2	US-09-248-796A-19630	Sequence 19630, A
162	56.5	12.3	757	2	US-09-949-016-7121	Sequence 7121, Ap	235	55	11.9	404	2	US-09-538-092-50	Sequence 50, Appl
163	56.5	12.3	852	1	US-08-190-802A-59	Sequence 59, Appl	236	55	11.9	406	2	US-09-252-991A-20630	Sequence 20630, A
164	56.5	12.3	852	1	US-08-130-802A-67	Sequence 67, Appl	237	55	11.9	459	2	US-08-311-731A-47	Sequence 47, Appl
165	56.5	12.3	852	2	US-08-477-346-59	Sequence 59, Appl	238	55	11.9	478	1	US-08-456-670B-40	Sequence 40, Appl
166	56.5	12.3	852	2	US-08-477-346-67	Sequence 67, Appl	239	55	11.9	478	2	US-09-372-036-40	Sequence 40, Appl
167	56.5	12.3	852	2	US-08-473-089-59	Sequence 59, Appl	240	55	11.9	484	1	US-08-127-499A-26	Sequence 26, Appl
168	56.5	12.3	852	2	US-08-473-089-67	Sequence 67, Appl	241	55	11.9	484	1	US-08-482-847-26	Sequence 26, Appl
169	56.5	12.3	852	2	US-08-487-072A-59	Sequence 59, Appl	242	55	11.9	512	1	US-08-173-508-4	Sequence 4, Appl
170	56.5	12.3	852	2	US-08-487-072A-67	Sequence 67, Appl	243	55	11.9	512	1	US-08-565-310-4	Sequence 4, Appl
171	56.5	12.3	884	2	US-09-520-781-6	Sequence 6, Appl	244	55	11.9	512	2	US-08-951-742-4	Sequence 4, Appl
172	56.5	12.3	884	2	US-09-957-187-6	Sequence 6, Appl	245	55	11.9	533	2	US-09-549-519-32	Sequence 32, Appl
173	56.5	12.3	884	2	US-09-991-053-6	Sequence 6, Appl	246	55	11.9	598	2	US-09-352-991A-25875	Sequence 25875, A



247	55	11.9	666	1	US-08-083-590A-17	Sequence 17, Appl	320	54	11.7	377	4	PCT-US94-07280-17	Sequence 17, Appl
248	55	11.9	666	1	US-08-346-128-36	Sequence 36, Appl	321	54	11.7	377	4	PCT-US95-01087-17	Sequence 17, Appl
249	55	11.9	666	2	US-05-532-364-17	Sequence 17, Appl	322	54	11.7	395	2	US-09-540-236-2520	Sequence 2520, Ap
250	55	11.9	1481	1	US-08-616-844-40	Sequence 40, Appl	323	54	11.7	397	1	US-08-188-281B-11	Sequence 11, Appl
251	55	11.9	1481	1	US-08-599-654-40	Sequence 40, Appl	324	54	11.7	397	4	PCT-US94-07280-11	Sequence 11, Appl
252	55	11.9	1481	2	US-08-944-868A-40	Sequence 40, Appl	325	54	11.7	397	4	PCT-US95-01087-11	Sequence 11, Appl
253	55	11.9	1481	2	US-08-944-423A-40	Sequence 40, Appl	326	54	11.7	410	1	US-08-188-281B-18	Sequence 18, Appl
254	55	11.9	1481	2	US-08-944-496-40	Sequence 40, Appl	327	54	11.7	410	1	PCT-US94-07280-18	Sequence 18, Appl
255	54.5	11.9	102	2	US-09-540-236-2816	Sequence 2816, Ap	328	54	11.7	410	2	PCT-US95-01087-18	Sequence 18, Appl
256	54.5	11.8	139	2	US-09-270-767-32364	Sequence 32364, A	329	54	11.7	412	2	US-09-489-039A-9118	Sequence 9118, Ap
257	54.5	11.8	139	2	US-09-270-767-47581	Sequence 47581, A	330	54	11.7	417	1	US-08-188-281B-19	Sequence 19, Appl
258	54.5	11.8	221	2	US-09-270-767-31937	Sequence 31937, A	331	54	11.7	417	4	PCT-US94-07280-19	Sequence 19, Appl
259	54.5	11.8	221	2	US-09-270-767-47154	Sequence 47154, A	332	54	11.7	417	4	PCT-US95-01087-19	Sequence 19, Appl
260	54.5	11.8	240	2	US-09-902-540-11028	Sequence 11028, A	333	54	11.7	434	1	US-08-188-281B-10	Sequence 10, Appl
261	54.5	11.8	251	2	US-08-875-811-59	Sequence 59, Appl	334	54	11.7	434	4	PCT-US94-07280-10	Sequence 10, Appl
262	54.5	11.8	267	2	US-09-634-238-278	Sequence 278, App	335	54	11.7	434	4	PCT-US95-01087-10	Sequence 10, Appl
263	54.5	11.8	384	1	US-08-675-650B-4	Sequence 4, Appli	336	54	11.7	441	1	US-08-188-281B-21	Sequence 21, Appl
264	54.5	11.8	384	1	US-08-675-650B-6	Sequence 6, Appli	337	54	11.7	441	1	PCT-US94-07280-21	Sequence 21, Appl
265	54.5	11.8	384	2	US-08-907-608-2	Sequence 2, Appli	338	54	11.7	441	4	PCT-US95-01087-21	Sequence 21, Appl
266	54.5	11.8	384	2	US-08-907-608-4	Sequence 4, Appli	339	54	11.7	443	2	US-09-461-325-147	Sequence 147, App
267	54.5	11.8	384	2	US-09-059-769-10	Sequence 10, Appl	340	54	11.7	443	2	US-10-012-542-147	Sequence 147, App
268	54.5	11.8	384	2	US-09-354-231B-2	Sequence 2, Appli	341	54	11.7	443	2	US-10-115-123-147	Sequence 147, App
269	54.5	11.8	384	2	US-09-354-231B-4	Sequence 4, Appli	342	54	11.7	447	1	US-08-188-281B-20	Sequence 20, Appl
270	54.5	11.8	384	2	US-09-128-602B-2	Sequence 2, Appli	343	54	11.7	447	4	PCT-US94-07280-20	Sequence 20, Appl
271	54.5	11.8	384	2	US-09-128-602B-4	Sequence 4, Appli	344	54	11.7	447	4	PCT-US95-01087-20	Sequence 20, Appl
272	54.5	11.8	384	2	US-09-482-287-2	Sequence 2, Appli	345	54	11.7	453	1	US-08-188-281B-16	Sequence 16, Appl
273	54.5	11.8	384	2	US-09-482-287-4	Sequence 4, Appli	346	54	11.7	453	1	PCT-US94-07280-16	Sequence 16, Appl
274	54.5	11.8	384	2	US-09-966-888-2	Sequence 2, Appli	347	54	11.7	453	4	PCT-US95-01087-16	Sequence 16, Appl
275	54.5	11.8	384	2	US-09-966-888-4	Sequence 4, Appli	348	54	11.7	478	2	US-09-489-039A-7367	Sequence 7367, Ap
276	54.5	11.8	384	2	US-09-995-297-2	Sequence 2, Appli	349	54	11.7	490	1	US-08-188-281B-15	Sequence 15, Appl
277	54.5	11.8	384	2	US-09-995-297-4	Sequence 4, Appli	350	54	11.7	490	4	PCT-US94-07280-15	Sequence 15, Appl
278	54.5	11.8	426	2	US-09-902-540-12232	Sequence 12232, A	351	54	11.7	490	4	PCT-US95-01087-15	Sequence 15, Appl
279	54.5	11.8	446	2	US-09-543-681A-5864	Sequence 5864, Ap	352	54	11.7	493	2	US-09-170-984-2	Sequence 2, Appli
280	54.5	11.8	477	2	US-09-489-039A-10570	Sequence 10570, A	353	54	11.7	518	2	US-09-540-236-3648	Sequence 3648, Ap
281	54.5	11.8	481	2	US-09-724-623-77	Sequence 77, Appl	354	54	11.7	580	2	US-09-538-032-601	Sequence 601, App
282	54.5	11.8	613	2	US-09-328-352-7962	Sequence 7962, Ap	355	54	11.7	891	2	US-09-252-991A-28689	Sequence 28689, A
283	54.5	11.8	631	2	US-09-328-352-6860	Sequence 6860, Ap	356	54	11.7	1036	2	US-09-902-540-14218	Sequence 14218, A
284	54.5	11.8	752	1	US-08-281-193-2	Sequence 2, Appli	357	54	11.7	3623	2	US-09-341-461-2	Sequence 2, Appli
285	54.5	11.8	752	1	US-08-422-106-2	Sequence 2, Appli	358	53.5	11.6	72	2	US-09-188-930-182	Sequence 182, App
286	54.5	11.8	752	1	US-08-735-716-2	Sequence 2, Appli	359	53.5	11.6	221	2	US-09-464-535-22	Sequence 22, Appl
287	54.5	11.8	752	1	US-08-555-568B-2	Sequence 2, Appli	360	53.5	11.6	244	1	US-08-361-395-1	Sequence 1, Appli
288	54.5	11.8	752	2	US-09-519-223-2	Sequence 2, Appli	361	53.5	11.6	244	2	US-09-618-259-11	Sequence 11, Appl
289	54.5	11.8	752	2	US-09-927-180-2	Sequence 2, Appli	362	53.5	11.6	272	2	US-09-583-110-3866	Sequence 3866, Ap
290	54.5	11.8	752	4	PCT-US95-08069-2	Sequence 2, Appli	363	53.5	11.6	284	2	US-09-902-540-16417	Sequence 16417, A
291	54.5	11.8	765	2	US-09-949-016-7844	Sequence 7844, Ap	364	53.5	11.6	302	2	US-09-252-991A-21655	Sequence 21655, A
292	54.5	11.8	780	2	US-08-280-690-2	Sequence 2, Appli	365	53.5	11.6	308	2	US-09-489-039A-14278	Sequence 14278, A
293	54.5	11.8	781	1	US-08-123-161A-8	Sequence 8, Appli	366	53.5	11.6	310	2	US-09-107-433-1601	Sequence 4601, Ap
294	54.5	11.8	895	1	US-08-483-278-8	Sequence 8, Appli	367	53.5	11.6	325	2	US-09-949-016-7713	Sequence 7713, Ap
295	54.5	11.8	895	1	US-09-949-016-6490	Sequence 6490, Ap	368	53.5	11.6	359	2	US-08-637-670-37	Sequence 37, Appl
296	54.5	11.8	895	2	US-09-949-016-7178	Sequence 7178, Ap	369	53.5	11.6	382	2	US-09-489-039A-13696	Sequence 13696, A
297	54.5	11.8	920	2	US-09-949-016-7178	Sequence 7178, Ap	370	53.5	11.6	407	2	US-09-710-279-1578	Sequence 1578, Ap
298	54	11.7	135	1	US-08-188-281B-6	Sequence 6, Appli	371	53.5	11.6	410	1	US-08-723-415B-10	Sequence 10, Appl
299	54	11.7	135	4	PCT-US94-07280-6	Sequence 6, Appli	372	53.5	11.6	410	2	US-09-189-827A-10	Sequence 10, Appl
300	54	11.7	135	4	PCT-US95-01087-6	Sequence 6, Appli	373	53.5	11.6	410	2	US-09-710-861-10	Sequence 10, Appl
301	54	11.7	172	1	US-08-188-281B-5	Sequence 5, Appli	374	53.5	11.6	415	2	US-09-349-016-8808	Sequence 8808, Ap
302	54	11.7	172	4	PCT-US94-07280-5	Sequence 5, Appli	375	53.5	11.6	437	2	US-09-350-841A-1591	Sequence 1591, Ap
303	54	11.7	172	4	PCT-US95-01087-5	Sequence 5, Appli	376	53.5	11.6	438	2	US-08-486-099-105	Sequence 105, App
304	54	11.7	178	2	US-09-936-588-42	Sequence 42, Appl	377	53.5	11.6	438	2	US-08-360-107A-115	Sequence 115, App
305	54	11.7	221	1	US-08-188-281B-2	Sequence 2, Appli	378	53.5	11.6	438	2	US-08-484-223B-105	Sequence 105, App
306	54	11.7	221	4	PCT-US94-07280-2	Sequence 2, Appli	379	53.5	11.6	438	2	US-08-919-597-105	Sequence 105, App
307	54	11.7	221	4	PCT-US95-01087-2	Sequence 2, Appli	380	53.5	11.6	438	2	US-08-475-668A-105	Sequence 105, App
308	54	11.7	241	2	US-09-005-238-46	Sequence 46, Appl	381	53.5	11.6	438	2	US-08-471-913A-105	Sequence 105, App
309	54	11.7	241	2	US-08-768-619-46	Sequence 46, Appl	382	53.5	11.6	438	2	US-08-485-264A-105	Sequence 105, App
310	54	11.7	346	2	US-09-702-705-329	Sequence 329, App	383	53.5	11.6	438	2	US-08-474-349A-105	Sequence 105, App
311	54	11.7	346	2	US-09-736-457-329	Sequence 329, App	384	53.5	11.6	438	2	US-08-470-896-105	Sequence 105, App
312	54	11.7	346	2	US-09-614-124B-329	Sequence 329, App	385	53.5	11.6	438	2	US-08-485-546A-105	Sequence 105, App
313	54	11.7	346	2	US-09-671-325-329	Sequence 329, App	386	53.5	11.6	438	2	US-08-487-266A-105	Sequence 105, App
314	54	11.7	346	2	US-09-589-184-329	Sequence 329, App	387	53.5	11.6	438	2	US-08-484-741-105	Sequence 105, App
315	54	11.7	346	2	US-09-658-824-329	Sequence 329, App	388	53.5	11.6	440	2	US-09-134-001C-3286	Sequence 3286, Ap
316	54	11.7	346	2	US-10-017-754-329	Sequence 329, App	389	53.5	11.6	495	2	US-09-275-252A-5	Sequence 5, Appli
317	54	11.7	346	2	US-09-651-563-329	Sequence 329, App	390	53.5	11.6	550	1	US-09-279-700-16	Sequence 16, Appl
318	54	11.7	346	2	US-09-519-642-329	Sequence 329, App	391	53.5	11.6	550	1	US-08-230-944-18	Sequence 18, Appl
319	54	11.7	377	1	US-08-188-281B-17	Sequence 17, Appl	392	53.5	11.6	550	2	US-09-230-944-18	Sequence 18, Appl

393	53.5	11.6	550	2	US-09-230-944-20	Sequence 20, Appl	466	52.5	11.4	384	2	US-09-128-602B-12	Sequence 12, Appl
394	53.5	11.6	550	2	US-09-873-233A-18	Sequence 18, Appl	467	52.5	11.4	384	2	US-09-482-287-6	Sequence 6, Appl
395	53.5	11.6	550	2	US-09-873-233A-20	Sequence 20, Appl	468	52.5	11.4	384	2	US-09-966-888-6	Sequence 6, Appl
396	53.5	11.6	550	2	US-10-149-634-2	Sequence 2, Appl	469	52.5	11.4	384	2	US-09-995-297-6	Sequence 6, Appl
397	53.5	11.6	898	2	US-10-149-315-11	Sequence 11, Appl	470	52.5	11.4	384	2	US-09-995-297-8	Sequence 8, Appl
398	53	11.5	68	2	US-09-243-675-3	Sequence 3, Appl	471	52.5	11.4	384	2	US-09-995-297-10	Sequence 10, Appl
399	53	11.5	115	78	US-09-749-637A-228	Sequence 228, App	472	52.5	11.4	384	2	US-09-995-297-12	Sequence 12, Appl
400	53	11.5	165	2	US-10-104-047-2538	Sequence 2538, App	473	52.5	11.4	384	2	US-09-697-379-4	Sequence 4, Appl
401	53	11.5	223	2	US-09-605-703B-2326	Sequence 2326, Ap	474	52.5	11.4	384	2	US-10-116-212A-4	Sequence 4, Appl
402	53	11.5	225	2	US-08-543-681A-4579	Sequence 4579, Ap	475	52.5	11.4	396	2	US-09-198-452A-147	Sequence 147, App
403	53	11.5	239	2	US-08-913-014A-2	Sequence 2, Appl	476	52.5	11.4	410	1	US-08-723-415B-11	Sequence 11, Appl
404	53	11.5	239	2	US-09-653-285-2	Sequence 2, Appl	477	52.5	11.4	410	1	US-08-428-131-2	Sequence 2, Appl
405	53	11.5	299	2	US-09-252-991A-24215	Sequence 24215, A	478	52.5	11.4	410	1	US-08-602-846-2	Sequence 2, Appl
406	53	11.5	319	2	US-09-134-000C-6061	Sequence 6061, Ap	479	52.5	11.4	410	2	US-09-189-596-2	Sequence 2, Appl
407	53	11.5	348	2	US-09-134-001C-4857	Sequence 4857, Ap	480	52.5	11.4	410	2	US-09-189-627A-11	Sequence 11, Appl
408	53	11.5	355	2	US-09-902-540-14706	Sequence 14706, A	481	52.5	11.4	410	2	US-09-710-861-11	Sequence 11, Appl
409	53	11.5	356	2	US-09-664-840-2	Sequence 2, Appl	482	52.5	11.4	435	2	US-09-489-039A-13740	Sequence 13740, A
410	53	11.5	377	1	US-08-188-277B-4	Sequence 4, Appl	483	52.5	11.4	448	2	US-09-328-352-5807	Sequence 5807, Ap
411	53	11.5	377	1	US-08-429-964-78	Sequence 78, Appl	484	52.5	11.4	468	2	US-09-602-787A-612	Sequence 612, App
412	53	11.5	377	2	US-09-538-092-1199	Sequence 1199, Ap	485	52.5	11.4	483	2	US-09-949-016-7773	Sequence 7773, Ap
413	53	11.5	407	2	US-09-489-039A-13350	Sequence 13350, A	486	52.5	11.4	523	2	US-09-538-092-571	Sequence 571, App
414	53	11.5	454	2	US-09-949-016-10198	Sequence 10198, A	487	52.5	11.4	525	2	US-08-888-949-16	Sequence 16, Appl
415	53	11.5	460	2	US-09-489-039A-13505	Sequence 13505, A	488	52.5	11.4	525	2	US-08-888-950-16	Sequence 16, Appl
416	53	11.5	469	2	US-09-902-540-12213	Sequence 12213, A	489	52.5	11.4	525	2	US-09-262-758-16	Sequence 16, Appl
417	53	11.5	474	2	US-09-489-039A-10791	Sequence 10791, A	490	52.5	11.4	525	2	US-09-885-876-16	Sequence 16, Appl
418	53	11.5	476	2	US-09-489-039A-12217	Sequence 12217, A	491	52.5	11.4	525	2	US-09-885-901-16	Sequence 16, Appl
419	53	11.5	482	2	US-09-438-185A-356	Sequence 356, App	492	52.5	11.4	525	2	US-09-731-393-16	Sequence 16, Appl
420	53	11.5	524	2	US-09-549-519-27	Sequence 27, Appl	493	52.5	11.4	550	2	US-09-120-365-1	Sequence 1, Appl
421	53	11.5	524	2	US-09-549-519-28	Sequence 28, Appl	494	52.5	11.4	550	2	US-09-515-039-1	Sequence 1, Appl
422	53	11.5	563	2	US-09-949-016-8277	Sequence 8277, Ap	495	52.5	11.4	609	2	US-09-107-532A-5110	Sequence 5110, Ap
423	53	11.5	574	2	US-09-248-796A-16849	Sequence 16849, A	496	52.5	11.4	693	2	US-09-949-016-9666	Sequence 9666, Ap
424	53	11.5	580	2	US-09-489-039A-8096	Sequence 8096, Ap	497	52.5	11.4	706	2	US-09-252-991A-25730	Sequence 25730, A
425	53	11.5	605	2	US-09-902-540-12393	Sequence 12393, A	498	52.5	11.4	763	2	US-10-104-047-2766	Sequence 2766, Ap
426	53	11.5	661	2	US-09-540-236-3743	Sequence 3743, Ap	499	52.5	11.4	800	2	US-09-489-039A-10358	Sequence 10358, A
427	53	11.5	678	2	US-09-252-991A-20202	Sequence 20202, A	500	52.5	11.4	801	2	US-09-543-681A-7561	Sequence 7561, Ap
428	53	11.5	686	2	US-09-252-991A-19332	Sequence 19332, A	501	52.5	11.4	969	2	US-09-321-987B-5	Sequence 5, Appl
429	53	11.5	792	2	US-09-995-587A-11	Sequence 11, Appl	502	52.5	11.4	1000	2	US-09-352-159-25	Sequence 25, Appl
430	53	11.5	896	2	US-09-585-858-17	Sequence 17, Appl	503	52.5	11.4	1000	2	US-09-352-168-25	Sequence 25, Appl
431	53	11.5	896	2	US-10-270-878-17	Sequence 17, Appl	504	52.5	11.4	1000	2	US-09-771-045B-25	Sequence 25, Appl
432	53	11.5	1016	2	US-09-232-991A-18914	Sequence 18914, A	505	52.5	11.4	1000	2	US-09-770-564B-25	Sequence 25, Appl
433	53	11.5	1070	2	US-09-961-403-3	Sequence 3, Appl	506	52.5	11.4	1000	2	US-09-658-835C-25	Sequence 25, Appl
434	53	11.5	1146	2	US-09-834-734-2	Sequence 2, Appl	507	52.5	11.4	1101	2	US-08-331-625A-52	Sequence 52, Appl
435	53	11.5	1238	2	US-09-904-065-2	Sequence 2, Appl	508	52.5	11.4	1101	2	US-08-331-625A-54	Sequence 54, Appl
436	53	11.5	1238	2	US-09-904-065-14	Sequence 14, Appl	509	52.5	11.4	1101	2	US-09-494-151-52	Sequence 52, Appl
437	53	11.5	1240	1	US-08-680-326-37	Sequence 37, Appl	510	52.5	11.4	1101	2	US-09-494-151-54	Sequence 54, Appl
438	53	11.5	1240	2	US-09-904-065-4	Sequence 4, Appl	511	52.5	11.4	1101	2	US-09-972-484-52	Sequence 52, Appl
439	53	11.5	1240	2	US-09-904-065-15	Sequence 15, Appl	512	52.5	11.4	1101	2	US-09-972-484-54	Sequence 54, Appl
440	53	11.5	1336	2	US-09-949-016-6806	Sequence 6806, Ap	513	52.5	11.4	1205	2	US-09-491-522-11	Sequence 11, Appl
441	53	11.5	1339	2	US-09-949-016-10448	Sequence 10448, A	514	52.5	11.4	1279	2	US-09-489-039A-13602	Sequence 13602, A
442	53	11.5	1478	2	US-09-949-016-8315	Sequence 8315, Ap	515	52.5	11.4	1452	2	US-08-331-625A-2	Sequence 2, Appl
443	52.5	11.4	21	2	US-09-962-756-592	Sequence 592, App	516	52.5	11.4	1452	2	US-09-494-151-2	Sequence 2, Appl
444	52.5	11.4	71	2	US-09-369-247-79	Sequence 79, Appl	517	52.5	11.4	1452	4	US-09-972-484-2	Sequence 2, Appl
445	52.5	11.4	71	2	US-10-062-548-79	Sequence 79, Appl	518	52.5	11.4	1452	4	PCT-US93-04384-18	Sequence 18, Appl
446	52.5	11.4	123	2	US-09-107-532A-4652	Sequence 4652, Ap	519	52.5	11.4	1452	4	PCT-US93-04692-2	Sequence 2, Appl
447	52.5	11.4	126	2	US-08-331-625A-9	Sequence 9, Appl	520	52.5	11.4	1453	1	US-08-308-872B-6	Sequence 6, Appl
448	52.5	11.4	126	2	US-09-494-151-9	Sequence 9, Appl	521	52.5	11.4	2037	2	US-09-306-998-3	Sequence 3, Appl
449	52.5	11.4	126	2	US-09-972-484-9	Sequence 9, Appl	522	52.5	11.4	2046	2	US-09-949-016-9365	Sequence 9365, Ap
450	52.5	11.4	158	2	US-09-464-535-8	Sequence 8, Appl	523	52	11.3	87	2	US-09-252-991A-17552	Sequence 17552, A
451	52.5	11.4	167	2	US-09-438-185A-132	Sequence 132, App	524	52	11.3	105	2	US-09-388-143-209	Sequence 209, App
452	52.5	11.4	216	2	US-09-464-535-28	Sequence 28, Appl	525	52	11.3	127	2	US-09-328-352-4209	Sequence 4209, Ap
453	52.5	11.4	236	2	US-09-270-767-44948	Sequence 44948, A	526	52	11.3	132	2	US-09-454-279-6	Sequence 6, Appl
454	52.5	11.4	251	2	US-08-331-625A-59	Sequence 59, Appl	527	52	11.3	136	2	US-09-270-767-39814	Sequence 39814, A
455	52.5	11.4	251	2	US-09-494-151-59	Sequence 59, Appl	528	52	11.3	136	2	US-09-370-767-55031	Sequence 55031, A
456	52.5	11.4	251	2	US-09-972-484-59	Sequence 59, Appl	529	52	11.3	160	2	US-09-583-110-5206	Sequence 5206, Ap
457	52.5	11.4	384	2	US-09-907-608-6	Sequence 6, Appl	530	52	11.3	161	2	US-09-107-433-3565	Sequence 3565, Ap
458	52.5	11.4	384	2	US-08-354-231B-6	Sequence 6, Appl	531	52	11.3	175	2	US-09-270-767-46710	Sequence 46710, A
459	52.5	11.4	384	2	US-09-354-231B-8	Sequence 8, Appl	532	52	11.3	216	2	US-09-107-532A-3711	Sequence 3711, Ap
460	52.5	11.4	384	2	US-09-354-231B-10	Sequence 10, Appl	533	52	11.3	231	2	US-09-303-518D-432	Sequence 432, App
461	52.5	11.4	384	2	US-09-354-231B-12	Sequence 12, Appl	534	52	11.3	260	2	US-09-025-059-3	Sequence 3, Appl
462	52.5	11.4	384	2	US-09-133-962A-4	Sequence 4, Appl	535	52	11.3	260	2	US-08-888-429A-26	Sequence 26, Appl
463	52.5	11.4	384	2	US-09-128-602B-6	Sequence 6, Appl	536	52	11.3	260	2	US-09-593-653-26	Sequence 26, Appl
464	52.5	11.4	384	2	US-09-128-602B-8	Sequence 8, Appl	537	52	11.3	260	2	US-09-618-259-8	Sequence 8, Appl
465	52.5	11.4	384	2	US-09-128-602B-10	Sequence 10, Appl	538	52	11.3	261	2	US-09-454-279-16	Sequence 16, Appl

539	52	11.3	262	2	US-09-303-518D-434	Sequence 434, App	612	51.5	11.2	307	2	US-10-015-671A-95	Sequence 95, Appl
540	52	11.3	267	2	US-09-248-796A-17580	Sequence 17580, A	613	51.5	11.2	307	2	US-10-015-833A-95	Sequence 95, Appl
541	52	11.3	304	2	US-09-543-681A-7290	Sequence 7290, Ap	614	51.5	11.2	307	2	US-10-011-833A-95	Sequence 95, Appl
542	52	11.3	312	2	US-09-543-681A-6689	Sequence 6689, Ap	615	51.5	11.2	307	2	US-10-006-041A-95	Sequence 95, Appl
543	52	11.3	336	2	US-09-902-540-10582	Sequence 10582, A	616	51.5	11.2	307	2	US-10-012-064A-95	Sequence 95, Appl
544	52	11.3	350	2	US-09-543-681A-4618	Sequence 4618, Ap	617	51.5	11.2	319	2	US-08-581-148C-12	Sequence 12, Appl
545	52	11.3	371	2	US-09-949-016-8635	Sequence 8635, Ap	618	51.5	11.2	334	1	US-08-118-270-73	Sequence 73, Appl
546	52	11.3	380	2	US-08-888-429A-30	Sequence 30, Appl	619	51.5	11.2	334	4	PCT-US93-08528-73	Sequence 73, Appl
547	52	11.3	380	2	US-09-593-653-20	Sequence 30, Appl	620	51.5	11.2	369	1	US-08-416-756A-2	Sequence 2, Appl
548	52	11.3	387	2	US-08-252-991A-22112	Sequence 22112, A	621	51.5	11.2	369	2	US-08-880-865-2	Sequence 2, Appl
549	52	11.3	389	2	US-08-888-429A-20	Sequence 20, Appl	622	51.5	11.2	371	2	US-09-949-016-9073	Sequence 9073, Ap
550	52	11.3	389	2	US-09-593-653-20	Sequence 20, Appl	623	51.5	11.2	381	1	US-08-845-366-3	Sequence 3, Appl
551	52	11.3	415	2	US-09-543-681A-6292	Sequence 6292, Ap	624	51.5	11.2	381	1	US-08-467-948A-28	Sequence 28, Appl
552	52	11.3	419	2	US-08-888-429A-28	Sequence 28, Appl	625	51.5	11.2	381	2	US-08-852-824-18	Sequence 18, Appl
553	52	11.3	419	2	US-09-446-754-6	Sequence 6, Appl	626	51.5	11.2	381	2	US-08-467-947A-28	Sequence 28, Appl
554	52	11.3	419	2	US-08-166-166-2	Sequence 2, Appl	627	51.5	11.2	381	2	US-09-731-030A-17	Sequence 17, Appl
555	52	11.3	419	2	US-09-206-166-5	Sequence 5, Appl	628	51.5	11.2	381	2	US-09-518-383-18	Sequence 18, Appl
556	52	11.3	419	2	US-09-593-653-28	Sequence 28, Appl	629	51.5	11.2	381	4	PCT-US96-10618-4	Sequence 4, Appl
557	52	11.3	420	1	US-08-864-804-1	Sequence 1, Appl	630	51.5	11.2	382	2	US-09-542-733-2	Sequence 2, Appl
558	52	11.3	433	2	US-09-949-016-7636	Sequence 7636, Ap	631	51.5	11.2	382	2	US-09-262-477-2	Sequence 2, Appl
559	52	11.3	435	2	US-08-446-754-2	Sequence 2, Appl	632	51.5	11.2	382	2	US-09-169-205D-21	Sequence 21, Appl
560	52	11.3	453	2	US-08-888-429A-32	Sequence 32, Appl	633	51.5	11.2	383	1	US-08-196-989B-4	Sequence 4, Appl
561	52	11.3	453	2	US-09-593-653-32	Sequence 32, Appl	634	51.5	11.2	383	1	US-08-760-326-4	Sequence 4, Appl
562	52	11.3	468	2	US-09-446-754-4	Sequence 4, Appl	635	51.5	11.2	383	2	US-09-225-024-4	Sequence 4, Appl
563	52	11.3	468	2	US-09-446-754-10	Sequence 10, Appl	636	51.5	11.2	384	2	US-08-530-862B-4	Sequence 4, Appl
564	52	11.3	475	2	US-09-949-016-11570	Sequence 11570, A	637	51.5	11.2	384	2	US-08-597-313D-4	Sequence 4, Appl
565	52	11.3	482	2	US-08-489-039A-9909	Sequence 9909, Ap	638	51.5	11.2	384	2	US-09-885-189-4	Sequence 4, Appl
566	52	11.3	521	2	US-08-669-656A-4	Sequence 4, Appl	639	51.5	11.2	390	1	US-08-416-756A-5	Sequence 5, Appl
567	52	11.3	596	2	US-09-134-001C-3363	Sequence 3363, Ap	640	51.5	11.2	390	2	US-08-880-865-5	Sequence 5, Appl
568	52	11.3	628	2	US-09-602-787A-550	Sequence 550, App	641	51.5	11.2	407	2	US-08-733-007A-6	Sequence 6, Appl
569	52	11.3	628	2	US-09-602-787A-666	Sequence 666, App	642	51.5	11.2	407	2	US-09-398-496-6	Sequence 6, Appl
570	52	11.3	736	2	US-09-252-991A-19048	Sequence 19048, A	643	51.5	11.2	429	2	US-08-311-731A-287	Sequence 287, App
571	52	11.3	1194	2	US-08-949-016-9803	Sequence 9803, Ap	644	51.5	11.2	453	2	US-09-540-336-3464	Sequence 3464, Ap
572	52	11.3	1195	2	US-09-949-016-6535	Sequence 6535, Ap	645	51.5	11.2	495	2	US-09-270-767-44726	Sequence 44726, A
573	52	11.3	1666	2	US-09-949-016-8322	Sequence 8322, Ap	646	51.5	11.2	509	2	US-08-845-546-2	Sequence 2, Appl
574	52	11.3	1956	2	US-08-843-417-2	Sequence 2, Appl	647	51.5	11.2	511	2	US-09-252-991A-27306	Sequence 27306, A
575	52	11.3	1956	2	US-09-527-013-2	Sequence 2, Appl	648	51.5	11.2	522	2	US-09-549-519-40	Sequence 40, Appl
576	52	11.3	1957	2	US-08-669-656A-2	Sequence 2, Appl	649	51.5	11.2	549	2	US-09-345-473E-32	Sequence 32, Appl
577	52	11.3	1957	2	US-08-669-656A-8	Sequence 8, Appl	650	51.5	11.2	549	2	US-09-862-027-32	Sequence 32, Appl
578	52	11.3	2057	2	US-09-499-203-2	Sequence 2, Appl	651	51.5	11.2	550	1	US-08-348-891A-5	Sequence 5, Appl
579	52	11.3	2132	2	US-08-669-656A-6	Sequence 6, Appl	652	51.5	11.2	550	1	US-08-905-817-5	Sequence 5, Appl
580	51.5	11.2	115	2	US-09-513-999C-7866	Sequence 7866, Ap	653	51.5	11.2	550	2	US-10-149-634-4	Sequence 4, Appl
581	51.5	11.2	123	1	US-08-180-209B-19	Sequence 19, Appl	654	51.5	11.2	563	2	US-10-046-232-24	Sequence 24, Appl
582	51.5	11.2	123	1	US-08-385-745-19	Sequence 19, Appl	655	51.5	11.2	567	2	US-09-252-991A-28481	Sequence 28481, A
583	51.5	11.2	123	2	US-08-485-388-19	Sequence 19, Appl	656	51.5	11.2	586	2	US-09-489-039A-10912	Sequence 10912, A
584	51.5	11.2	123	2	US-08-474-853-19	Sequence 19, Appl	657	51.5	11.2	586	2	US-09-252-991A-18033	Sequence 18033, A
585	51.5	11.2	123	2	US-08-166-205B-19	Sequence 19, Appl	658	51.5	11.2	630	2	US-09-228-986-80	Sequence 80, Appl
586	51.5	11.2	123	2	PCT-US94-02629-19	Sequence 2234, Ap	659	51.5	11.2	707	2	US-10-101-464A-80	Sequence 80, Appl
587	51.5	11.2	123	4	US-09-949-016-9179	Sequence 1756, Ap	660	51.5	11.2	707	2	US-09-589-892B-11	Sequence 11, Appl
588	51.5	11.2	134	2	US-08-605-703B-1756	Sequence 20175, A	661	51.5	11.2	808	2	US-10-104-047-2654	Sequence 2654, Ap
589	51.5	11.2	185	2	US-08-252-991A-20175	Sequence 20175, A	662	51.5	11.2	848	2	US-08-976-255-10	Sequence 10, Appl
590	51.5	11.2	187	2	US-09-949-016-9179	Sequence 9179, Ap	663	51.5	11.2	869	1	US-08-483-101-15	Sequence 15, Appl
591	51.5	11.2	211	2	US-09-130-491-4	Sequence 4, Appl	664	51.5	11.2	1451	1	US-08-308-872B-4	Sequence 4, Appl
592	51.5	11.2	211	2	US-09-603-552-12	Sequence 12, Appl	665	51.5	11.2	1451	2	US-08-332-459-32	Sequence 32, Appl
593	51.5	11.2	211	2	US-09-886-683A-4	Sequence 4, Appl	666	51.5	11.2	1454	2	US-09-854-799-32	Sequence 32, Appl
594	51.5	11.2	211	2	US-09-949-016-6992	Sequence 6992, Ap	667	51.5	11.2	1454	4	PCT-US91-08525-32	Sequence 32, Appl
595	51.5	11.2	211	2	US-09-998-833A-270	Sequence 270, App	668	51.5	11.2	1454	4	PCT-US93-04384-12	Sequence 12, Appl
596	51.5	11.2	211	2	US-10-020-445A-270	Sequence 270, App	669	51.5	11.2	1454	4	PCT-US93-04384-44	Sequence 44, Appl
597	51.5	11.2	212	1	US-08-461-859-35	Sequence 35, Appl	670	51.5	11.2	1454	4	PCT-US93-04384-46	Sequence 46, Appl
598	51.5	11.2	212	2	US-09-917-254-62	Sequence 62, Appl	671	51.5	11.2	1454	4	PCT-US93-04384-47	Sequence 47, Appl
599	51.5	11.2	224	2	US-08-871-572B-13	Sequence 13, Appl	672	51.5	11.2	2539	2	US-09-413-814-42	Sequence 42, Appl
600	51.5	11.2	240	2	US-09-252-991A-30410	Sequence 30410, A	673	51	11.1	86	2	US-08-654-737B-2	Sequence 2, Appl
601	51.5	11.2	241	2	US-10-076-069-4	Sequence 4, Appl	674	51	11.1	109	2	US-09-198-452A-11	Sequence 11, Appl
602	51.5	11.2	247	2	US-09-949-016-11579	Sequence 11579, A	675	51	11.1	109	2	US-09-438-185A-2	Sequence 2, Appl
603	51.5	11.2	250	2	US-09-167-717-1	Sequence 1, Appl	676	51	11.1	109	2	US-09-270-767-32131	Sequence 32131, A
604	51.5	11.2	268	2	US-09-818-780-17	Sequence 17, Appl	677	51	11.1	119	2	US-09-543-681A-6396	Sequence 6396, Ap
605	51.5	11.2	268	2	US-09-818-780-94	Sequence 94, Appl	678	51	11.1	141	2	US-09-605-703B-1998	Sequence 1998, Ap
606	51.5	11.2	292	2	US-09-205-258-1116	Sequence 1116, Ap	679	51	11.1	205	2	US-08-248-796A-20685	Sequence 20685, A
607	51.5	11.2	292	2	US-10-004-860-1116	Sequence 1116, Ap	680	51	11.1	211	2	US-08-277-231A-14	Sequence 14, Appl
608	51.5	11.2	307	2	US-09-107-433-4181	Sequence 4181, Ap	681	51	11.1	214	1	US-08-473-750-3	Sequence 3, Appl
609	51.5	11.2	307	2	US-10-012-231A-95	Sequence 95, Appl	682	51	11.1	214	1	US-08-477-326-3	Sequence 3, Appl
610	51.5	11.2	307	2	US-10-015-389A-95	Sequence 95, Appl	683	51	11.1	217	1	US-08-277-231A-12	Sequence 2, Appl
611	51.5	11.2	307	2	US-10-006-768A-95	Sequence 95, Appl	684	51	11.1	217	1	US-08-277-231A-12	Sequence 12, Appl

685	51	11.1	217	1	US-08-473-750-1	Sequence 1, Appli	758	50.5	11.0	326	2	US-09-328-352-5506	Sequence 5506, Ap
686	51	11.1	217	1	US-08-473-750-5	Sequence 5, Appli	759	50.5	11.0	349	2	US-09-949-016-9786	Sequence 9786, Ap
687	51	11.1	217	1	US-08-477-326-1	Sequence 5, Appli	760	50.5	11.0	355	2	US-08-984-618-14	Sequence 14, Appl
688	51	11.1	217	1	US-08-477-326-5	Sequence 1, Appli	761	50.5	11.0	355	2	US-09-829-275-1	Sequence 1, Appli
689	51	11.1	222	2	US-09-252-991A-29014	Sequence 29014, A	762	50.5	11.0	377	1	US-08-188-277B-2	Sequence 2, Appli
690	51	11.1	230	2	US-09-328-352-7370	Sequence 7370, Ap	763	50.5	11.0	377	1	US-08-429-964-80	Sequence 80, Appl
691	51	11.1	294	2	US-09-252-991A-27242	Sequence 27242, A	764	50.5	11.0	385	2	US-09-107-532A-5871	Sequence 5871, Ap
692	51	11.1	301	2	US-09-489-039A-12748	Sequence 12748, A	765	50.5	11.0	411	2	US-09-107-532A-6966	Sequence 6966, Ap
693	51	11.1	320	2	US-09-902-540-12563	Sequence 12563, A	766	50.5	11.0	424	2	US-09-902-540-10575	Sequence 10575, A
694	51	11.1	321	2	US-09-290-586A-22	Sequence 22, Appl	767	50.5	11.0	424	2	US-09-902-540-14942	Sequence 14942, A
695	51	11.1	326	2	US-09-489-039A-11901	Sequence 11901, A	768	50.5	11.0	433	2	US-09-902-540-13296	Sequence 13296, A
696	51	11.1	328	2	US-09-489-039A-10986	Sequence 10986, A	769	50.5	11.0	442	2	US-09-538-092-637	Sequence 637, App
697	51	11.1	330	2	US-09-134-001C-3815	Sequence 3815, Ap	770	50.5	11.0	455	2	US-09-543-681A-7043	Sequence 7043, Ap
698	51	11.1	338	2	US-09-949-016-8751	Sequence 8751, Ap	771	50.5	11.0	461	2	US-09-107-532A-5964	Sequence 5964, Ap
699	51	11.1	346	2	US-08-888-429A-18	Sequence 18, Appl	772	50.5	11.0	467	2	US-09-902-540-11298	Sequence 11298, A
700	51	11.1	346	2	US-09-198-452A-60	Sequence 60, Appl	773	50.5	11.0	476	2	US-10-142-835-28	Sequence 28, Appl
701	51	11.1	354	2	US-09-593-653-18	Sequence 18, Appl	774	50.5	11.0	477	2	US-09-252-991A-29825	Sequence 29825, A
702	51	11.1	356	2	US-09-902-540-15411	Sequence 15411, A	775	50.5	11.0	499	2	US-09-252-991A-27221	Sequence 27221, A
703	51	11.1	361	1	US-08-390-162-4	Sequence 4, Appli	776	50.5	11.0	529	1	US-07-891-942G-8	Sequence 8, Appli
704	51	11.1	361	1	US-08-685-945B-4	Sequence 4, Appli	777	50.5	11.0	529	1	US-08-370-909-19	Sequence 19, Appl
705	51	11.1	365	1	US-08-390-162-2	Sequence 2, Appli	778	50.5	11.0	529	1	US-08-504-048-8	Sequence 8, Appli
706	51	11.1	365	1	US-08-685-945B-2	Sequence 2, Appli	779	50.5	11.0	529	2	US-09-341-982-1	Sequence 1, Appli
707	51	11.1	365	2	US-09-949-016-9075	Sequence 9075, Ap	780	50.5	11.0	529	2	US-09-169-717E-39	Sequence 39, Appl
708	51	11.1	370	2	US-09-489-039A-11515	Sequence 11515, A	781	50.5	11.0	529	2	US-10-011-436-4	Sequence 4, Appli
709	51	11.1	380	2	US-09-902-540-15775	Sequence 15775, A	782	50.5	11.0	529	2	US-08-533-895A-39	Sequence 39, Appl
710	51	11.1	383	2	US-08-530-862B-7	Sequence 7, Appli	783	50.5	11.0	537	2	US-08-540-922D-12	Sequence 12, Appl
711	51	11.1	384	2	US-08-597-313D-7	Sequence 7, Appli	784	50.5	11.0	550	1	US-08-279-700-18	Sequence 18, Appl
712	51	11.1	384	2	US-08-885-189-7	Sequence 7, Appli	785	50.5	11.0	550	1	US-08-279-700-20	Sequence 20, Appl
713	51	11.1	430	2	US-09-902-540-12684	Sequence 12684, A	786	50.5	11.0	550	1	US-08-279-700-22	Sequence 22, Appl
714	51	11.1	438	2	US-09-107-532A-5677	Sequence 5677, Ap	787	50.5	11.0	560	1	US-07-891-942G-5	Sequence 5, Appli
715	51	11.1	451	2	US-09-489-039A-8949	Sequence 8949, Ap	788	50.5	11.0	566	2	US-09-491-522-7	Sequence 7, Appli
716	51	11.1	475	2	US-09-489-039A-8862	Sequence 8862, Ap	789	50.5	11.0	566	2	US-09-949-016-7010	Sequence 7010, Ap
717	51	11.1	485	2	US-10-140-372-12	Sequence 12, Appl	790	50.5	11.0	566	2	US-09-949-016-8505	Sequence 8505, Ap
718	51	11.1	485	2	US-08-438-185A-43	Sequence 43, Appl	791	50.5	11.0	566	2	US-09-949-002-452	Sequence 452, App
719	51	11.1	490	2	US-09-438-185A-1032	Sequence 1032, Ap	792	50.5	11.0	586	2	US-09-252-991A-22589	Sequence 22589, A
720	51	11.1	534	2	US-09-605-703B-1142	Sequence 1142, Ap	793	50.5	11.0	614	2	US-09-949-016-10772	Sequence 10772, A
721	51	11.1	584	2	US-09-107-532A-4564	Sequence 4564, Ap	794	50.5	11.0	757	2	US-09-902-540-11380	Sequence 11380, A
722	51	11.1	590	2	US-09-248-796A-26874	Sequence 26874, A	795	50.5	11.0	867	2	US-09-839-894-6	Sequence 6, Appli
723	51	11.1	598	2	US-09-248-796A-19190	Sequence 19190, A	796	50.5	11.0	974	2	US-08-938-291A-4	Sequence 4, Appli
724	51	11.1	677	2	US-08-252-991A-20406	Sequence 20406, A	797	50.5	11.0	974	2	US-09-589-619-4	Sequence 4, Appli
725	51	11.1	749	1	US-08-046-508-2	Sequence 2, Appli	798	50.5	11.0	1106	2	US-09-134-000C-6136	Sequence 6136, Ap
726	51	11.1	749	2	US-09-250-083C-2	Sequence 2, Appli	799	50.5	11.0	1163	1	US-08-173-497-4	Sequence 4, Appli
727	51	11.1	822	2	US-08-248-796A-19917	Sequence 19917, A	800	50.5	11.0	1163	1	US-08-286-889-4	Sequence 4, Appli
728	51	11.1	866	1	US-08-386-727-8	Sequence 8, Appli	801	50.5	11.0	1163	1	US-08-485-618-4	Sequence 4, Appli
729	51	11.1	866	1	US-08-600-452A-8	Sequence 8, Appli	802	50.5	11.0	1163	1	US-08-362-652-4	Sequence 4, Appli
730	51	11.1	954	2	US-09-854-845-14	Sequence 14, Appl	803	50.5	11.0	1163	1	US-08-605-672-4	Sequence 4, Appli
731	51	11.1	967	2	US-09-139-802-201	Sequence 201, App	804	50.5	11.0	1163	1	US-08-482-263A-4	Sequence 4, Appli
732	51	11.1	967	2	US-09-659-786-201	Sequence 201, App	805	50.5	11.0	1163	1	US-08-943-363-4	Sequence 4, Appli
733	51	11.1	1049	2	US-09-854-845-2	Sequence 2, Appli	806	50.5	11.0	1163	2	US-08-476-62A-44	Sequence 44, Appli
734	51	11.1	1093	2	US-09-854-845-4	Sequence 4, Appli	807	50.5	11.0	1163	2	US-09-193-043-4	Sequence 4, Appli
735	51	11.1	1151	2	US-09-854-845-10	Sequence 10, Appl	808	50.5	11.0	1163	2	US-09-688-307A-4	Sequence 4, Appli
736	51	11.1	1479	2	US-08-840-062-4	Sequence 4, Appli	809	50.5	11.0	1163	2	US-09-350-259-4	Sequence 4, Appli
737	51	11.1	1956	2	US-08-843-417-10	Sequence 10, Appl	810	50.5	11.0	1211	2	PCT-US96-01314-44	Sequence 44, Appl
738	51	11.1	1956	2	US-08-527-013-10	Sequence 10, Appl	811	50.5	11.0	1211	2	US-09-431-522-5	Sequence 5, Appli
739	50.5	11.0	26	2	US-09-962-756-1658	Sequence 1658, Ap	812	50.5	11.0	1211	2	US-09-949-016-11401	Sequence 11401, A
740	50.5	11.0	87	2	US-09-605-703B-960	Sequence 960, App	813	50.5	11.0	1211	2	US-09-949-002-401	Sequence 401, App
741	50.5	11.0	87	2	US-09-605-703B-962	Sequence 962, App	814	50.5	11.0	1211	2	US-09-949-002-555	Sequence 555, App
742	50.5	11.0	142	2	US-10-104-047-2706	Sequence 2706, Ap	815	50.5	11.0	1245	2	US-09-252-991A-30935	Sequence 30935, A
743	50.5	11.0	147	2	US-09-543-681A-4506	Sequence 4506, Ap	816	50.5	11.0	1317	2	US-09-083-521-7	Sequence 7, Appli
744	50.5	11.0	188	1	US-08-160-524A-5	Sequence 5, Appli	817	50.5	11.0	2703	1	US-08-185-432-19	Sequence 19, Appl
745	50.5	11.0	207	1	US-08-609-443B-15	Sequence 15, Appl	818	50.5	11.0	2703	2	US-08-899-232-4	Sequence 4, Appli
746	50.5	11.0	207	1	US-08-569-063C-15	Sequence 15, Appl	819	50.5	11.0	2703	1	US-09-121-457-4	Sequence 4, Appli
747	50.5	11.0	207	2	US-08-851-896-15	Sequence 15, Appl	820	50.5	11.0	3169	1	US-08-477-451-6	Sequence 6, Appli
748	50.5	11.0	249	2	US-08-851-896-15	Sequence 15, Appl	821	50	10.8	31	2	US-09-270-767-37409	Sequence 7, Appli
749	50.5	11.0	249	2	US-09-602-777A-344	Sequence 344, App	822	50	10.8	31	2	US-09-270-767-52626	Sequence 2626, A
750	50.5	11.0	254	2	US-09-107-433-4333	Sequence 4333, Ap	823	50	10.8	69	2	US-09-248-796A-27038	Sequence 27038, A
751	50.5	11.0	255	2	US-09-605-703B-244	Sequence 244, App	824	50	10.8	92	2	US-09-127-946-8	Sequence 8, Appli
752	50.5	11.0	263	2	US-09-605-703B-242	Sequence 242, App	825	50	10.8	92	2	US-10-191-732-8	Sequence 8, Appli
753	50.5	11.0	264	1	US-08-463-115-93	Sequence 93, Appl	826	50	10.8	93	2	US-09-148-545-256	Sequence 256, App
754	50.5	11.0	264	1	US-08-463-388-93	Sequence 93, Appl	827	50	10.8	93	2	US-09-621-011-256	Sequence 256, App
755	50.5	11.0	271	2	US-08-252-991A-18965	Sequence 18965, A	828	50	10.8	102	2	US-09-198-452A-475	Sequence 475, App
756	50.5	11.0	304	2	US-09-902-540-13353	Sequence 13353, A	829	50	10.8	105	2	US-09-248-796A-19711	Sequence 19711, A
757	50.5	11.0	306	2	US-09-252-991A-22181	Sequence 22181, A	830	50	10.8	119	2	US-09-482-273-264	Sequence 264, App

831	50	10.8	147	2	US-09-902-540-12970	Sequence 12970, A	904	49.5	10.7	252	2	US-09-976-994-582	Sequence 582, App
832	50	10.8	195	2	US-09-394-142B-16	Sequence 16, Appl	905	49.5	10.7	252	2	US-09-919-439-228	Sequence 228, App
833	50	10.8	201	2	US-09-270-767-31650	Sequence 31650, A	906	49.5	10.7	262	2	US-09-134-001C-3746	Sequence 3746, Ap
834	50	10.8	201	2	US-09-270-767-46867	Sequence 46867, A	907	49.5	10.7	262	2	US-09-710-279-1568	Sequence 1568, Ap
835	50	10.8	248	2	US-09-634-238-279	Sequence 279, App	908	49.5	10.7	265	2	US-09-780-016-8	Sequence 8, Appl
836	50	10.8	252	2	US-09-902-540-12546	Sequence 12546, A	909	49.5	10.7	265	2	US-10-214-811-8	Sequence 8, Appl
837	50	10.8	261	2	US-09-543-681A-5280	Sequence 5280, Ap	910	49.5	10.7	265	2	US-10-766-074-8	Sequence 8, Appl
838	50	10.8	263	2	US-09-328-352-4486	Sequence 4486, Ap	911	49.5	10.7	268	2	US-09-716-964B-156	Sequence 156, App
839	50	10.8	264	2	US-09-198-452A-266	Sequence 266, App	912	49.5	10.7	290	2	US-09-780-016-6	Sequence 6, Appl
840	50	10.8	267	2	US-09-134-000C-6206	Sequence 6206, Ap	913	49.5	10.7	290	2	US-10-214-811-6	Sequence 6, Appl
841	50	10.8	273	2	US-09-489-039A-12374	Sequence 12374, A	914	49.5	10.7	290	2	US-10-766-074-6	Sequence 6, Appl
842	50	10.8	277	2	US-09-303-518D-400	Sequence 400, App	915	49.5	10.7	296	2	US-09-489-847-293	Sequence 293, App
843	50	10.8	279	2	US-09-134-001C-4878	Sequence 4878, Ap	916	49.5	10.7	315	2	US-09-107-532A-5917	Sequence 5917, Ap
844	50	10.8	303	2	US-09-543-681A-5154	Sequence 5154, Ap	917	49.5	10.7	319	2	US-09-252-991A-28066	Sequence 28066, A
845	50	10.8	308	1	US-08-164-232B-18	Sequence 18, Appl	918	49.5	10.7	320	2	US-09-489-039A-10349	Sequence 10349, A
846	50	10.8	308	2	US-08-845-623-18	Sequence 18, Appl	919	49.5	10.7	322	2	US-09-949-016-11381	Sequence 11381, A
847	50	10.8	308	2	US-08-815-927-18	Sequence 18, Appl	920	49.5	10.7	324	2	US-09-602-787A-484	Sequence 484, App
848	50	10.8	308	2	US-09-103-330-18	Sequence 18, Appl	921	49.5	10.7	328	2	US-09-605-703B-2840	Sequence 2840, Ap
849	50	10.8	308	2	US-09-435-242-18	Sequence 18, Appl	922	49.5	10.7	353	2	US-09-489-039A-12270	Sequence 12270, A
850	50	10.8	322	2	US-09-252-991A-24657	Sequence 24657, A	923	49.5	10.7	363	2	US-09-949-016-11040	Sequence 11040, A
851	50	10.8	323	2	US-09-107-532A-6263	Sequence 6263, Ap	924	49.5	10.7	364	2	US-09-489-039A-10066	Sequence 10066, A
852	50	10.8	326	2	US-09-784-810C-11	Sequence 11, Appl	925	49.5	10.7	372	1	US-08-626-685A-8	Sequence 8, Appl
853	50	10.8	356	2	US-09-125-619-2	Sequence 2, Appl	926	49.5	10.7	372	2	US-08-993-088A-2	Sequence 2, Appl
854	50	10.8	356	2	US-09-125-619-13	Sequence 13, Appl	927	49.5	10.7	372	2	US-08-993-088A-20	Sequence 20, Appl
855	50	10.8	356	2	US-10-222-566-2	Sequence 2, Appl	928	49.5	10.7	372	2	US-08-993-424B-2	Sequence 2, Appl
856	50	10.8	356	2	US-10-222-566-13	Sequence 13, Appl	929	49.5	10.7	372	2	US-08-665-034A-2	Sequence 4, Appl
857	50	10.8	356	2	US-10-143-044A-2	Sequence 2, Appl	930	49.5	10.7	372	2	US-08-665-034A-4	Sequence 4, Appl
858	50	10.8	356	2	US-10-143-044A-13	Sequence 13, Appl	931	49.5	10.7	372	2	US-09-595-549-9	Sequence 9, Appl
859	50	10.8	356	2	US-10-222-162-2	Sequence 2, Appl	932	49.5	10.7	372	2	US-09-603-680-2	Sequence 2, Appl
860	50	10.8	356	2	US-10-222-162-13	Sequence 13, Appl	933	49.5	10.7	372	2	US-09-603-680-20	Sequence 20, Appl
861	50	10.8	358	2	US-09-270-767-45037	Sequence 45037, A	934	49.5	10.7	372	2	US-08-981-700A-2	Sequence 2, Appl
862	50	10.8	378	2	US-09-902-540-11860	Sequence 11860, A	935	49.5	10.7	372	2	US-08-899-112B-8	Sequence 8, Appl
863	50	10.8	390	2	US-09-710-279-1422	Sequence 1422, Ap	936	49.5	10.7	378	2	US-09-011-553-2	Sequence 2, Appl
864	50	10.8	427	2	US-09-902-540-15413	Sequence 15413, A	937	49.5	10.7	378	2	US-09-689-486-62	Sequence 62, Appl
865	50	10.8	436	2	US-08-584-760A-1	Sequence 67, Appl	938	49.5	10.7	380	2	US-09-120-355-76	Sequence 76, Appl
866	50	10.8	440	2	US-08-584-760A-1	Sequence 1, Appl	939	49.5	10.7	380	2	US-09-515-039-76	Sequence 76, Appl
867	50	10.8	447	2	US-10-163-012-29	Sequence 29, Appl	940	49.5	10.7	380	2	US-08-860-255A-5	Sequence 5, Appl
868	50	10.8	461	2	US-09-543-681A-6448	Sequence 6448, Ap	941	49.5	10.7	394	2	US-09-710-279-3292	Sequence 3292, Ap
869	50	10.8	468	2	US-09-498-612-6	Sequence 6, Appl	942	49.5	10.7	403	2	US-09-489-039A-11022	Sequence 11022, A
870	50	10.8	471	2	US-09-784-810C-6	Sequence 6, Appl	943	49.5	10.7	414	2	US-09-710-279-806	Sequence 806, App
871	50	10.8	501	2	US-09-252-991A-31885	Sequence 31885, A	944	49.5	10.7	420	2	US-08-252-991A-30428	Sequence 30428, A
872	50	10.8	521	2	US-09-134-001C-4290	Sequence 4290, Ap	945	49.5	10.7	423	2	US-09-134-001C-3599	Sequence 3599, Ap
873	50	10.8	525	2	US-09-949-016-7407	Sequence 7407, Ap	946	49.5	10.7	427	2	US-09-328-352-6602	Sequence 6602, Ap
874	50	10.8	533	2	US-09-549-519-31	Sequence 31, Appl	947	49.5	10.7	436	2	US-09-502-540-9717	Sequence 9717, Ap
875	50	10.8	544	2	US-09-252-991A-26096	Sequence 26096, A	948	49.5	10.7	462	2	US-09-886-319A-72	Sequence 72, Appl
876	50	10.8	605	2	US-09-949-016-8269	Sequence 8269, Ap	949	49.5	10.7	469	2	US-08-753-007A-8	Sequence 8, Appl
877	50	10.8	606	2	US-09-538-092-798	Sequence 798, App	950	49.5	10.7	469	2	US-09-398-496-8	Sequence 8, Appl
878	50	10.8	641	2	US-09-653-274-13	Sequence 13, Appl	951	49.5	10.7	470	2	US-10-104-047-3775	Sequence 3775, Ap
879	50	10.8	641	2	US-10-461-791-13	Sequence 13, Appl	952	49.5	10.7	476	2	US-09-134-001C-3778	Sequence 3778, Ap
880	50	10.8	772	2	US-09-252-991A-30446	Sequence 30446, A	953	49.5	10.7	498	2	US-09-248-796A-15018	Sequence 15018, A
881	50	10.8	1070	2	US-09-653-274-8	Sequence 8, Appl	954	49.5	10.7	507	2	US-09-780-016-2	Sequence 2, Appl
882	50	10.8	1070	2	US-10-461-791-8	Sequence 8, Appl	955	49.5	10.7	507	2	US-10-214-811-2	Sequence 2, Appl
883	50	10.8	1086	2	US-09-653-274-4	Sequence 4, Appl	956	49.5	10.7	507	2	US-10-766-074-2	Sequence 2, Appl
884	50	10.8	1086	2	US-10-461-791-4	Sequence 4, Appl	957	49.5	10.7	532	2	US-09-780-016-20	Sequence 20, Appl
885	50	10.8	1309	2	US-09-862-027-82	Sequence 82, Appl	958	49.5	10.7	532	2	US-10-214-811-20	Sequence 20, Appl
886	50	10.8	1381	2	US-08-826-134-4	Sequence 4, Appl	959	49.5	10.7	532	2	US-09-907-794A-259	Sequence 259, App
887	50	10.8	1443	1	US-08-308-872B-2	Sequence 2, Appl	960	49.5	10.7	556	2	US-09-905-125A-259	Sequence 259, App
888	50	10.8	1479	2	US-08-840-062-2	Sequence 2, Appl	961	49.5	10.7	556	2	US-09-902-775A-259	Sequence 259, App
889	49.5	10.7	58	1	US-09-513-999C-6346	Sequence 6346, Ap	962	49.5	10.7	556	2	US-09-903-603A-259	Sequence 259, App
890	49.5	10.7	66	2	US-09-513-999C-7224	Sequence 7224, Ap	963	49.5	10.7	556	2	US-09-904-920A-259	Sequence 259, App
891	49.5	10.7	160	2	US-09-732-210-304	Sequence 304, App	964	49.5	10.7	556	2	US-09-904-920A-259	Sequence 259, App
892	49.5	10.7	172	2	US-08-772-270A-1	Sequence 11, Ap	965	49.5	10.7	556	2	US-09-905-064-259	Sequence 259, App
893	49.5	10.7	172	2	US-08-772-270A-1	Sequence 1, Appl	966	49.5	10.7	556	2	US-09-905-381A-259	Sequence 259, App
894	49.5	10.7	172	2	US-09-062-126-2	Sequence 2, Appl	967	49.5	10.7	556	2	US-09-906-618-259	Sequence 259, App
895	49.5	10.7	193	2	US-09-475-316A-78	Sequence 78, Appl	968	49.5	10.7	556	2	US-09-906-646-259	Sequence 259, App
896	49.5	10.7	193	2	US-09-704-640-78	Sequence 78, Appl	969	49.5	10.7	556	2	US-09-904-462-259	Sequence 259, App
897	49.5	10.7	200	1	US-08-698-805-6	Sequence 6, Appl	970	49.5	10.7	556	2	US-09-902-736A-259	Sequence 259, App
898	49.5	10.7	212	2	US-09-813-453B-59	Sequence 59, Appl	971	49.5	10.7	556	2	US-09-906-722A-259	Sequence 259, App
899	49.5	10.7	246	2	US-09-134-001C-5292	Sequence 5292, Ap	972	49.5	10.7	557	2	US-10-771-708-4	Sequence 4, Appl
900	49.5	10.7	249	1	US-08-626-685A-11	Sequence 11, Appl	973	49.5	10.7	563	2	US-08-931-608A-3	Sequence 3, Appl
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902	49.5	10.7	249	2	US-07-885-089B-7	Sequence 7, Appl	975	49.5	10.7	563	2	US-09-252-991A-21510	Sequence 21510, A
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979	49.5	10.7	637	2	US-09-569-611C-35	Sequence 35, Appl	1052	49	10.6	349	2	US-09-134-001C-4004	Sequence 4004, Ap
980	49.5	10.7	647	2	US-09-398-496-32	Sequence 32, Appl	1053	49	10.6	352	2	US-08-466-343D-2	Sequence 2, Appli
981	49.5	10.7	647	2	US-09-398-496-32	Sequence 32, Appl	1054	49	10.6	352	2	US-09-087-232A-13	Sequence 13, Appl
982	49.5	10.7	647	2	US-09-907-794A-28	Sequence 28, Appl	1055	49	10.6	352	2	US-08-861-105-14	Sequence 14, Appl
983	49.5	10.7	660	2	US-09-905-125A-28	Sequence 28, Appl	1056	49	10.6	352	2	US-08-575-967A-2	Sequence 2, Appli
984	49.5	10.7	660	2	US-09-902-775A-28	Sequence 28, Appl	1057	49	10.6	352	2	US-09-045-583-52	Sequence 52, Appl
985	49.5	10.7	660	2	US-09-906-700-28	Sequence 28, Appl	1058	49	10.6	352	2	US-09-517-605-5	Sequence 5, Appli
986	49.5	10.7	660	2	US-09-903-603A-28	Sequence 28, Appl	1059	49	10.6	352	2	US-09-534-185-52	Sequence 52, Appl
987	49.5	10.7	660	2	US-09-904-920A-28	Sequence 28, Appl	1060	49	10.6	352	2	US-08-833-752-5	Sequence 5, Appli
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990	49.5	10.7	660	2	US-09-905-381A-28	Sequence 28, Appl	1063	49	10.6	352	2	US-09-938-719-5	Sequence 5, Appli
991	49.5	10.7	660	2	US-09-906-618-28	Sequence 28, Appl	1064	49	10.6	352	2	US-09-502-784A-2	Sequence 2, Appli
992	49.5	10.7	660	2	US-09-906-646-28	Sequence 28, Appl	1065	49	10.6	352	2	US-09-339-912A-2	Sequence 2, Appli
993	49.5	10.7	660	2	US-09-689-486-58	Sequence 58, Appl	1066	49	10.6	352	2	US-08-771-276-2	Sequence 2, Appli
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995	49.5	10.7	660	2	US-09-902-736A-28	Sequence 28, Appl	1068	49	10.6	352	2	US-09-939-226B-5	Sequence 5, Appli
996	49.5	10.7	660	2	US-09-906-722A-28	Sequence 28, Appl	1069	49	10.6	352	2	US-09-195-662A-2	Sequence 2, Appli
997	49.5	10.7	661	2	US-09-252-991A-27070	Sequence 27070, A	1070	49	10.6	352	2	US-09-949-002-303	Sequence 303, App
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1004	49	10.6	63	2	US-09-471-276-1429	Sequence 1429, Ap	1077	49	10.6	378	2	US-09-949-002-552	Sequence 552, App
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1006	49	10.6	103	2	US-09-543-681A-7951	Sequence 7951, Ap	1079	49	10.6	428	2	US-09-248-796A-20582	Sequence 20582, A
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1008	49	10.6	118	2	US-09-072-596-226	Sequence 226, App	1081	49	10.6	454	2	US-09-270-767-45646	Sequence 45646, A
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1010	49	10.6	118	2	US-10-193-002-226	Sequence 226, App	1083	49	10.6	463	2	US-09-252-991A-26212	Sequence 26212, A
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1019	49	10.6	195	2	US-09-231-818-24	Sequence 24, Appl	1092	49	10.6	526	2	US-09-328-352-8024	Sequence 8024, Ap
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1024	49	10.6	219	2	US-10-012-542-151	Sequence 151, App	1097	49	10.6	629	4	PCT-US92-09382-8	Sequence 8, Appli
1025	49	10.6	219	2	US-10-115-123-151	Sequence 151, App	1098	49	10.6	644	2	US-09-949-016-9507	Sequence 9507, Ap
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1124	49	10.6	914	2	US-09-133-562D-28	Sequence 28, Appl	1197	48.5	10.5	132	2	US-09-462-941-19	Sequence 19, Appl
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1126	49	10.6	914	2	US-10-055-412B-28	Sequence 28, Appl	1199	48.5	10.5	132	4	PCT-US93-07645A-2	Sequence 2, Appli
1127	49	10.6	914	2	US-10-270-595-6	Sequence 6, Appl	1200	48.5	10.5	132	4	PCT-US93-07645-2	Sequence 2, Appli
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1139	48.5	10.5	57	1	US-08-358-160-103	Sequence 103, App	1212	48.5	10.5	217	2	US-09-248-796A-19579	Sequence 19579, A
1140	48.5	10.5	77	2	US-08-311-731A-385	Sequence 385, App	1213	48.5	10.5	247	1	US-07-885-089B-8	Sequence 8, Appli
1141	48.5	10.5	94	2	US-08-252-991A-29771	Sequence 29771, A	1214	48.5	10.5	247	1	US-07-885-089B-8	Sequence 8, Appli
1142	48.5	10.5	112	1	US-08-284-333B-4	Sequence 4, Appli	1215	48.5	10.5	256	2	US-09-198-452A-449	Sequence 449, App
1143	48.5	10.5	112	1	US-08-284-333B-14	Sequence 14, Appl	1216	48.5	10.5	256	2	US-09-543-681A-4282	Sequence 4282, Ap
1144	48.5	10.5	112	4	PCT-US95-08950-4	Sequence 4, Appli	1217	48.5	10.5	257	2	US-09-438-185A-432	Sequence 432, App
1145	48.5	10.5	114	2	US-09-054-711C-4	Sequence 5, Appli	1218	48.5	10.5	257	2	US-08-665-402-5	Sequence 5, Appli
1146	48.5	10.5	114	2	US-09-054-711C-5	Sequence 5, Appli	1219	48.5	10.5	258	2	US-09-315-974-5	Sequence 5, Appli
1147	48.5	10.5	114	2	US-09-679-710B-1	Sequence 2, Appli	1220	48.5	10.5	279	2	US-09-328-352-4717	Sequence 4717, Ap
1148	48.5	10.5	114	2	US-09-679-710B-2	Sequence 2, Appli	1221	48.5	10.5	285	2	US-08-992-035A-1	Sequence 1, Appli
1149	48.5	10.5	114	2	US-09-679-710B-3	Sequence 3, Appli	1222	48.5	10.5	285	2	US-09-252-991A-32954	Sequence 32954, A
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1151	48.5	10.5	114	2	US-09-679-710B-5	Sequence 5, Appli	1224	48.5	10.5	293	2	US-09-314-701-44	Sequence 44, Appl
1152	48.5	10.5	114	2	US-09-679-710B-6	Sequence 6, Appli	1225	48.5	10.5	293	2	US-09-811-007A-40	Sequence 40, Appl
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1155	48.5	10.5	114	2	US-09-679-710B-9	Sequence 9, Appli	1228	48.5	10.5	300	2	US-09-489-039A-9673	Sequence 9673, Ap
1156	48.5	10.5	114	2	US-09-679-710B-10	Sequence 10, Appl	1229	48.5	10.5	304	2	US-09-902-540-9912	Sequence 9912, Ap
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1159	48.5	10.5	114	2	US-09-679-710B-13	Sequence 13, Appl	1232	48.5	10.5	361	2	US-09-902-540-10251	Sequence 10251, A
1160	48.5	10.5	114	2	US-09-679-710B-14	Sequence 14, Appl	1233	48.5	10.5	366	1	US-08-554-612C-50	Sequence 50, Appli
1161	48.5	10.5	114	2	US-09-679-710B-15	Sequence 15, Appl	1234	48.5	10.5	369	1	US-08-230-047-5	Sequence 5, Appli
1162	48.5	10.5	114	2	US-09-679-710B-16	Sequence 16, Appl	1235	48.5	10.5	404	2	US-10-104-047-3621	Sequence 3621, Ap
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1165	48.5	10.5	114	2	US-09-679-710B-19	Sequence 19, Appl	1238	48.5	10.5	450	2	US-09-489-039A-10052	Sequence 10052, A
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1169	48.5	10.5	114	2	US-09-679-710B-23	Sequence 23, Appl	1242	48.5	10.5	494	2	US-09-543-681A-7033	Sequence 7033, Ap
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1171	48.5	10.5	114	2	US-09-938-936-3	Sequence 3, Appli	1244	48.5	10.5	511	2	US-09-679-686B-12	Sequence 12, Appl
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1176	48.5	10.5	114	2	US-10-053-406-4	Sequence 5, Appli	1249	48.5	10.5	599	1	US-08-426-125-3	Sequence 3, Appli
1177	48.5	10.5	114	2	US-10-053-406-5	Sequence 6, Appli	1250	48.5	10.5	599	1	US-08-455-355-1	Sequence 1, Appli
1178	48.5	10.5	114	2	US-10-053-406-6	Sequence 7, Appli	1251	48.5	10.5	599	2	US-09-367-512-1	Sequence 1, Appli
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1180	48.5	10.5	114	2	US-10-053-406-8	Sequence 9, Appli	1253	48.5	10.5	638	1	US-09-769-787-8	Sequence 8, Appli
1181	48.5	10.5	114	2	US-10-053-406-9	Sequence 10, Appl	1254	48.5	10.5	638	1	US-08-426-125-4	Sequence 4, Appli
1182	48.5	10.5	114	2	US-10-053-406-10	Sequence 11, Appl	1255	48.5	10.5	638	2	US-08-455-355-4	Sequence 4, Appli
1183	48.5	10.5	114	2	US-10-053-406-11	Sequence 12, Appl	1256	48.5	10.5	638	2	US-09-367-512-3	Sequence 3, Appli
1184	48.5	10.5	114	2	US-10-053-406-12	Sequence 13, Appl	1257	48.5	10.5	638	2	US-10-407-339-3	Sequence 3, Appli
1185	48.5	10.5	114	2	US-10-053-406-13	Sequence 14, Appl	1258	48.5	10.5	655	2	US-09-134-001C-5531	Sequence 5531, Ap
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1193	48.5	10.5	114	2	US-10-053-406-21	Sequence 22, Appl	1266	48.5	10.5	1278	2	US-09-327-536-2	Sequence 2, Appli
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1271	48.5	10.5	4545	1	US-08-804-227C-14	Sequence 14, Appl	1344	48	10.4	362	2	US-09-949-016-8242	Sequence 8242, Ap
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1277	48	10.4	73	2	US-09-489-847-300	Sequence 300, App	1350	48	10.4	406	2	US-09-252-991A-28543	Sequence 28543, A
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1279	48	10.4	76	2	US-09-962-756-2182	Sequence 2182, Ap	1352	48	10.4	407	2	US-09-688-069-4	Sequence 4, Appli
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1281	48	10.4	120	2	US-09-931-381A-12	Sequence 12, Appl	1354	48	10.4	411	2	US-09-252-991A-30511	Sequence 30511, A
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1283	48	10.4	120	2	US-09-898-751A-14	Sequence 14, Appl	1356	48	10.4	417	2	US-09-857-612A-10	Sequence 10, Appl
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1285	48	10.4	133	2	US-10-206-576-226	Sequence 226, App	1358	48	10.4	425	2	US-09-328-352-7964	Sequence 7964, Ap
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1289	48	10.4	142	2	US-09-621-976-4460	Sequence 4460, Ap	1362	48	10.4	449	1	US-08-974-565C-1	Sequence 1, Appli
1290	48	10.4	143	2	US-09-857-612A-2	Sequence 2, Appli	1363	48	10.4	449	2	US-09-255-748-1	Sequence 1, Appli
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1298	48	10.4	187	2	US-09-270-767-32761	Sequence 32761, A	1371	48	10.4	500	2	US-09-596-377A-29	Sequence 29, Appl
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1302	48	10.4	192	2	US-09-704-640-87	Sequence 87, Appl	1375	48	10.4	503	2	US-09-487-558B-424	Sequence 424, App
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1304	48	10.4	206	2	US-09-096-724B-23	Sequence 23, Appl	1377	48	10.4	509	2	US-10-214-811-24	Sequence 24, Appl
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1316	48	10.4	239	2	US-10-015-393A-324	Sequence 324, App	1389	48	10.4	539	2	US-08-781-986A-5251	Sequence 5251, Ap
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1422	48	10.4	681	2	US-08-532-384-18	Sequence 18, Appli	1495	47.5	10.3	115	2	US-09-461-697-58	Sequence 58, Appli
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1443	48	10.4	858	2	US-10-237-551-92	Sequence 92, Appli							
1444	48	10.4	953	2	US-09-245-281-43	Sequence 43, Appli							
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1447	48	10.4	953	2	US-09-863-364-43	Sequence 43, Appli							
1448	48	10.4	953	2	US-09-728-721-43	Sequence 43, Appli							
1449	48	10.4	982	2	US-09-248-796A-20628	Sequence 20628, A							
1450	48	10.4	1001	2	US-10-415-147-3	Sequence 3, Appli							
1451	48	10.4	1078	1	US-08-264-534-32	Sequence 32, Appli							
1452	48	10.4	1078	1	US-08-083-590A-11	Sequence 11, Appli							
1453	48	10.4	1078	1	US-08-465-500-32	Sequence 32, Appli							
1454	48	10.4	1078	1	US-08-346-128-32	Sequence 32, Appli							
1455	48	10.4	1078	2	US-08-532-384-11	Sequence 11, Appli							
1456	48	10.4	1078	2	US-08-893-828-32	Sequence 32, Appli							
1457	48	10.4	1084	2	US-09-227-725A-3	Sequence 3, Appli							
1458	48	10.4	1084	2	US-10-071-900-3	Sequence 3, Appli							
1459	48	10.4	1225	2	US-09-501-171-4	Sequence 4, Appli							
1460	48	10.4	1225	2	US-09-949-016-6063	Sequence 6063, Ap							
1461	48	10.4	1244	2	US-09-902-540-9894	Sequence 9894, Ap							
1462	48	10.4	1478	2	US-09-487-558B-52	Sequence 52, Appli							
1463	48	10.4	1529	2	US-09-215-694-1	Sequence 1, Appli							
1464	48	10.4	1529	2	US-10-109-310-1	Sequence 1, Appli							
1465	48	10.4	1568	2	US-09-181-708-2	Sequence 2, Appli							
1466	48	10.4	1568	2	US-09-458-791-2	Sequence 2, Appli							
1467	48	10.4	1568	2	US-09-459-066-2	Sequence 2, Appli							
1468	48	10.4	1568	2	US-09-459-065-2	Sequence 2, Appli							
1469	48	10.4	1589	2	US-08-755-587-189	Sequence 189, App							
1470	48	10.4	1651	2	US-09-949-016-10643	Sequence 10643, A							
1471	48	10.4	1732	1	US-08-477-451-14	Sequence 14, Appli							
1472	48	10.4	1755	2	US-09-724-126A-6	Sequence 6, Appli							
1473	48	10.4	1850	2	US-09-620-093A-5	Sequence 5, Appli							
1474	48	10.4	2119	2	US-09-583-110-4893	Sequence 4893, Ap							
1475	48	10.4	2123	2	US-09-107-433-3728	Sequence 3728, Ap							
1476	48	10.4	2496	2	US-09-125-028-2	Sequence 2, Appli							
1477	48	10.4	2556	2	US-08-083-590A-20	Sequence 20, Appli							
1478	48	10.4	2556	2	US-08-532-384-20	Sequence 20, Appli							
1479	48	10.4	2958	2	US-08-894-344C-2	Sequence 2, Appli							
1480	48	10.4	2958	2	US-09-678-023A-2	Sequence 2, Appli							
1481	48	10.4	15281	1	US-08-471-119A-2	Sequence 2, Appli							
1482	47.5	10.3	65	2	US-09-962-756-2151	Sequence 2151, Ap							
1483	47.5	10.3	65	2	US-09-962-756-2185	Sequence 2185, Ap							
1484	47.5	10.3	75	2	US-08-924-629C-17	Sequence 17, Appli							
1485	47.5	10.3	75	2	US-08-924-629C-18	Sequence 18, Appli							
1486	47.5	10.3	83	2	US-09-962-756-2135	Sequence 2135, Ap							
1487	47.5	10.3	83	2	US-09-962-756-2150	Sequence 2150, Ap							

ALIGNMENTS

RESULT 1

US-09-289-349-11

; Sequence 11, Application US/09289349

; Patent No. 6277574

; GENERAL INFORMATION:

; APPLICANT: Walker, Michael, G.

; APPLICANT: Volkmut, Wayne

; APPLICANT: Klingner, Tod, M.

; APPLICANT: Azimzai, Yalda

; APPLICANT: Yue, Henry

; TITLE OF INVENTION: GENES ASSOCIATED WITH DISEASES OF THE KIDNEY

; FILE REFERENCE: PB-0010 US

; CURRENT APPLICATION NUMBER: US/09/289.349

; CURRENT FILING DATE: 1999-04-09

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PERL Program

; SEQ ID NO 11

; LENGTH: 89

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: 1900433CD1

US-09-289-349-11

Query Match 100.0%; Score 461; DB 2; Length 89;

Best Local Similarity 100.0%; Pred. No. 2e-51;

Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERVTLALLLAGLTALEANDPFANKDDPFYDWNKQLSGLICGGLLAIGIAVLSGK 60

Db 1 MERVTLALLLAGLTALEANDPFANKDDPFYDWNKQLSGLICGGLLAIGIAVLSGK 60

QY 61 CKYKSSQKHSPVPEKAIPITPGSATTC 89

Db 61 CKYKSSQKHSPVPEKAIPITPGSATTC 89

RESULT 2

US-09-991-181-262

; Sequence 262, Application US/09991181

; Patent No. 6913919

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C53  
CURRENT FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 461; DB 2; Length 89;  
Best Local Similarity 100.0%; Pred. No. 2e-51;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MERVTLALLLAGLTALEANDPFANKDDPFYDWKNLOSLGICGGLAIAAGIAVLGSK 60  
Db 1 MERVTLALLLAGLTALEANDPFANKDDPFYDWKNLOSLGICGGLAIAAGIAVLGSK 60  
Qy 61 CKYSSQKQHSVPPEKAIPITPGSATTC 89  
Db 61 CKYSSQKQHSVPPEKAIPITPGSATTC 89

RESULT 4  
US-09-997-333-262  
; Sequence 262, Application US/09997333  
; Patent No. 6953836  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Forgi, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gottard, Audrey E.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC27  
CURRENT APPLICATION NUMBER: US/09/997,333  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
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PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090435  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090472  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090535  
PRIOR FILING DATE: 1998-06-24  
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PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090676  
PRIOR FILING DATE: 1998-06-25

;; PRIOR APPLICATION NUMBER: 60/090678  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090690  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090694  
;; PRIOR FILING DATE: 1998-06-25  
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;; PRIOR FILING DATE: 1998-07-02  
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;; PRIOR APPLICATION NUMBER: 60/091978  
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;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 461; DB 2; Length 89;

Best Local Similarity 100.0%; Pred. No. 2e-51;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MERVTLALLLAGLTALEANDPFANKDDPFYYDKNLQSLICGGLATAGIAAVLSGK 60  
Db 1 MERVTLALLLAGLTALEANDPFANKDDPFYYDKNLQSLICGGLATAGIAAVLSGK 60

Qy 61 CKYSSQKQHSVPDEKAIPITPGSATTC 89  
Db 61 CKYSSQKQHSVPDEKAIPITPGSATTC 89

#### RESULT 5

US-09-992-598-262  
Sequence 262, Application US/09992598  
Patent No. 6956108  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey

;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730P1C20  
;; CURRENT FILING DATE: 2001-11-14  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
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;; PRIOR APPLICATION NUMBER: 60/088858  
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;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090678  
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;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090694  
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;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09  
Query Match 100.0%; Score 461; DB 2; Length 89;  
Best Local Similarity 100.0%; Pred. No. 2e-51;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MERVTLALLLAGLTALEANDPPANKDDPFYDWNKQLSGLICGGLLAIAAGIAVLGSK 60  
Db 1 MERVTLALLLAGLTALEANDPPANKDDPFYDWNKQLSGLICGGLLAIAAGIAVLGSK 60  
Qy 61 CKYKSSQKQHSVPPEKAIPITPGSATTC 89  
Db 61 CKYKSSQKQHSVPPEKAIPITPGSATTC 89

RESULT 6  
US-09-724-864-58  
; Sequence 58, Application US/09724864  
; Patent No. 6380362  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D  
; APPLICANT: Murison, James G.  
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed  
; TITLE OF INVENTION: by the polynucleotides and methods for their use.  
; FILE REFERENCE: 11000.105001  
; CURRENT APPLICATION NUMBER: US/09/724, 864  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 58  
; LENGTH: 88  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-724-864-58

Query Match 60.0%; Score 276.5; DB 2; Length 88;  
Best Local Similarity 66.7%; Pred. No. 9e-28;  
Matches 60; Conservative 8; Mismatches 19; Indels 3; Gaps 3;  
Qy 1 MERVTLA-LILLAGLTALEANDPPANKDDPFYDWNKQLSGLICGGLLAIAAGIAVLGSK 59  
Db 1 MEEITCAFLLLAGLPALEASDP-VDKDSPFYDWNESLQGLGGLIFGGLLCTAGIAAUSG 59





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; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/083,661
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0128 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 951423
; US-09-213-392-5

Query Match 55.6%; Score 256.5; DB 1; Length 87;
Best Local Similarity 61.5%; Pred.No.3.2e-25;
Matches 56; Conservative 11; Mismatches 17; Indels 7; Gaps 4;

QY 1 MERVTLA-LILLAGLTALANDPPYDKNQLQSLICGGLAIAGIAAVLSG 59
DB 1 MEGITCAFLVLVLAGLPVLEANGP-VDKGSPYYDWESLQLGMIFGSLLCIAGIAMALSG 59
QY 60 KCKYKSKQKHSP--VPEKAIPLTGSAAT 88
DB 60 KCK--CRNHTPSSLPEKVTPLITPGSAST 87

RESULT 10
US-09-083-661-5
; Sequence 5, Application US/09083661
; Patent No. 5955283
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/083,661
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,531
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0128 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 amino acids

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Qy 60 KCKYKSSQKQ-HSPVPEKAIPLIITPGSA 86  
Db 60 KCKCKFGQKSGHH--PGETPLIITPGSA 85

RESULT 12

US-08-725-531-4  
; Sequence 4, Application US/08725531  
; Patent No. 5756310  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Goli, Surya K.  
; TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/725,531  
; FILING DATE: Filed Herewith  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0128 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-845-4166  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 87 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 1085026

Qy 60 KCKYKSSQKQ-HSPVPEKAIPLIITPGSA 86  
Db 60 KCKCKFGQKSGHH--PGETPLIITPGSA 85

US-08-725-531-4

Query Match 46.5%; Score 214.5; DB 1; Length 87;  
Best Local Similarity 54.5%; Pred. No. 7.9e-20;  
Matches 48; Conservative 11; Mismatches 24; Indels 5; Gaps 4;  
Qy 1 MERVTLALLL-LAGLTALANDPFPYDKNLQSLGCGLLATAGIAAVLSG 59  
Db 1 MQKVTLLGLVFLAGFPVLDAND-LEDKNSPFYDWHSLQVGLGICAGVLCAMGIIVNSA 59

Qy 60 KCKYKSSQKQ-HSPVPEKAIPLIITPGSA 86  
Db 60 KCKCKFGQKSGHH--PGETPLIITPGSA 85

RESULT 13

US-08-738-127-4  
; Sequence 4, Application US/08738127  
; Patent No. 591855  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hawkins, Phillip R.  
; TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN HOMOLOG

Qy 60 KCKYKSSQKQ-HSPVPEKAIPLIITPGSA 86  
Db 60 KCKCKFGQKSGHH--PGETPLIITPGSA 85

RESULT 14

US-09-213-392-4  
; Sequence 4, Application US/09213392  
; Patent No. 5945505  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Goli, Surya K.  
; TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:

Qy 60 KCKYKSSQKQ-HSPVPEKAIPLIITPGSA 86  
Db 60 KCKCKFGQKSGHH--PGETPLIITPGSA 85

RESULT 15

US-08-738-127-4  
; Sequence 4, Application US/08738127  
; Patent No. 591855  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hawkins, Phillip R.  
; TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN HOMOLOG

NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: US  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/738,127  
FILING DATE: Filed Herewith  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0141 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 87 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 1085026  
US-08-738-127-4

Query Match 46.5%; Score 214.5; DB 1; Length 87;  
Best Local Similarity 54.5%; Pred. No. 7.9e-20;  
Matches 48; Conservative 11; Mismatches 24; Indels 5; Gaps 4;

Qy 1 MERVTLALLL-LAGLTALANDPFPYDKNLQSLGCGLLATAGIAAVLSG 59  
Db 1 MQKVTLLGLVFLAGFPVLDAND-LEDKNSPFYDWHSLQVGLGICAGVLCAMGIIVNSA 59

Qy 60 KCKYKSSQKQ-HSPVPEKAIPLIITPGSA 86  
Db 60 KCKCKFGQKSGHH--PGETPLIITPGSA 85

US-09-213-392-4  
; Sequence 4, Application US/09213392  
; Patent No. 5945505  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Goli, Surya K.  
; TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:

Qy 60 KCKYKSSQKQ-HSPVPEKAIPLIITPGSA 86  
Db 60 KCKCKFGQKSGHH--PGETPLIITPGSA 85

US-08-738-127-4  
; Sequence 4, Application US/08738127  
; Patent No. 591855  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hawkins, Phillip R.  
; TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN HOMOLOG

Qy 60 KCKYKSSQKQ-HSPVPEKAIPLIITPGSA 86  
Db 60 KCKCKFGQKSGHH--PGETPLIITPGSA 85

US-08-738-127-4

Query Match 46.5%; Score 214.5; DB 1; Length 87;  
Best Local Similarity 54.5%; Pred. No. 7.9e-20;  
Matches 48; Conservative 11; Mismatches 24; Indels 5; Gaps 4;  
Qy 1 MERVTLALLL-LAGLTALANDPFPYDKNLQSLGCGLLATAGIAAVLSG 59  
Db 1 MQKVTLLGLVFLAGFPVLDAND-LEDKNSPFYDWHSLQVGLGICAGVLCAMGIIVNSA 59

Qy 60 KCKYKSSQKQ-HSPVPEKAIPLIITPGSA 86  
Db 60 KCKCKFGQKSGHH--PGETPLIITPGSA 85

APPLICATION NUMBER: US/09/213,392  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/083,661  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PP-0128 US  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 87 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE: GenBank  
LIBRARY: GenBank  
CLONE: 1085026  
US-09-213-392-4

Query Match 46.5%; Score 214.5; DB 1; Length 87;  
Best Local Similarity 54.5%; Pred. No. 7.9e-20;  
Matches 48; Conservative 11; Mismatches 24; Indels 5; Gaps 4;  
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QY 60 KCKYKSSQKQ-HSPVPEKAIPITPGSA 86  
Db 60 KCKKFGQKSGHH--PGETPPLITPGSA 85

RESULT 15  
US-09-083-661-4  
Sequence 4, Application US/09083661  
Patent No. 5955283  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Goli, Surya K.  
TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/083,661  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/725,531  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PP-0128 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:

LENGTH: 87 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE: GenBank  
LIBRARY: GenBank  
CLONE: 1085026  
US-09-083-661-4  
Query Match 46.5%; Score 214.5; DB 1; Length 87;  
Best Local Similarity 54.5%; Pred. No. 7.9e-20;  
Matches 48; Conservative 11; Mismatches 24; Indels 5; Gaps 4;  
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Db 1 MQKVTGLLVFLAGFPVLDAND-LEDKNSPFYYDWHSLQVGGGLICAGVLCAMGIIIVWSA 59  
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Db 60 KCKKFGQKSGHH--PGETPPLITPGSA 85

Search completed: May 12, 2006, 21:30:05  
Job time : 69 secs

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OM protein - protein search, using sw model

Run on: May 12, 2006, 21:40:45 ; Search time 165 Seconds  
(without alignments)  
225.375 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications AA Main:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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741	461	100.0	89	5	US-10-972-317-50
742	461	100.0	89	5	US-10-820-474A-35
744	461	100.0	89	5	US-10-950-374-262
747	374	81.1	186	4	US-10-295-027-210
748	374	81.1	318	4	US-10-295-027-212
749	276.5	60.0	88	3	US-09-866-050A-698
750	276.5	60.0	87	4	US-10-176-847-24
751	214.5	46.5	87	4	US-10-205-823-140
752	214.5	46.5	87	4	US-10-177-293-166
753	214.5	46.5	87	4	US-10-295-027-1358
754	214.5	46.5	87	6	US-11-051-454-140
755	214.5	46.5	116	4	US-10-161-493-34
756	209.5	45.4	86	4	US-10-161-493-32
757	191.5	41.5	113	4	US-10-205-823-142
758	191.5	41.5	113	4	US-10-177-293-168
759	191.5	41.5	113	4	US-10-295-027-1357
760	191.5	41.5	113	6	US-11-051-454-142
761	191.5	41.5	150	3	US-09-925-299-955
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763	129	28.0	92	3	US-09-981-876-238
764	129	28.0	92	3	US-09-148-545-238
765	129	28.0	92	3	US-09-903-190-120
766	129	28.0	92	3	US-09-978-360A-776
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769	129	28.0	92	5	US-10-979-111-238	Sequence 238, App
770	129	28.0	93	3	US-09-981-876-183	Sequence 183, App
771	129	28.0	93	3	US-09-148-545-183	Sequence 183, App
772	129	28.0	93	5	US-10-979-111-183	Sequence 183, App
773	121	26.2	70	3	US-09-981-876-269	Sequence 269, App
774	121	26.2	70	3	US-09-148-545-269	Sequence 269, App
775	121	26.2	70	5	US-10-979-111-269	Sequence 269, App
776	113.5	24.6	138	4	US-10-291-265-446	Sequence 446, App
777	112.5	24.4	95	4	US-10-291-265-918	Sequence 918, App
778	112.5	24.4	96	3	US-09-809-391-473	Sequence 473, App
779	112.5	24.4	96	3	US-09-882-171-473	Sequence 473, App
780	112.5	24.4	96	4	US-10-164-861-473	Sequence 473, App
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782	112.5	24.4	120	5	US-10-931-886-434	Sequence 434, App
783	112.5	24.4	120	5	US-10-955-952-434	Sequence 434, App
784	112.5	24.4	120	5	US-10-950-374-199	Sequence 199, App
785	106	23.0	69	3	US-09-809-391-606	Sequence 606, App
786	1301	106	69	3	US-09-882-171-606	Sequence 606, App
787	1302	106	69	4	US-10-164-861-606	Sequence 606, App
788	1303	105.5	110	5	US-10-450-763-56705	Sequence 56705, A
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792	1307	94	178	3	US-09-985-153-93	Sequence 93, Appl
793	1308	94	178	3	US-09-985-153-94	Sequence 94, Appl
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Job time : 166 secs

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 12, 2006, 21:41:45 ; Search time 28 Seconds  
(without alignments)  
149.230 Million cell updates/sec

Perfect score: 461  
Sequence: 1 MERVTLALLAGLTALAN.....HSPVPEKAIPLITPGSATT 89

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 4694837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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11	214.5	46.5	87	9	US-10-475-075-192
12	214.5	46.5	87	9	US-10-475-075-476
13	214.5	46.5	87	11	US-11-080-991-24
14	129	28.0	92	7	US-09-978-360A-776
15	113.5	24.6	138	11	US-11-000-463-446
16	112.5	24.4	95	11	US-11-000-463-918
17	112.5	24.4	96	11	US-11-144-947-473
19	112.5	24.4	120	9	US-10-973-115B-434
22	112.5	24.4	120	11	US-11-290-153-434
23	106	23.0	69	11	US-11-144-947-606
25	94	20.4	178	9	US-10-821-234-1495
30	94	20.4	178	11	US-11-152-366-46
31	94	20.4	178	11	US-11-072-175-173
32	94	20.4	178	11	US-11-264-096-1532
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36	67.5	14.6	664	11	US-11-080-991-40
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					Sequence 192, Appl
					Sequence 476, Appl
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					Sequence 776, Appl
					Sequence 918, Appl
					Sequence 416, Appl
					Sequence 473, Appl
					Sequence 434, Appl
					Sequence 434, Appl
					Sequence 606, Appl
					Sequence 1495, Appl
					Sequence 173, Appl
					Sequence 163, Appl
					Sequence 1532, Appl
					Sequence 1531, Appl
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					Sequence 534, Appl
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37	66.5	14.4	523	11	US-11-288-493-10	Sequence 10, Appl
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39	63.5	13.8	309	11	US-11-045-004-1223	Sequence 1223, Ap
60	62.5	13.6	339	11	US-11-226-657-66	Sequence 66, Appl
61	62.5	13.6	340	11	US-11-226-657-174	Sequence 174, Appl
62	62	13.4	599	9	US-10-455-772-110	Sequence 110, App
63	62	13.4	605	9	US-10-455-772-106	Sequence 106, App
64	62	13.4	613	9	US-10-455-772-112	Sequence 112, App
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66	61.5	13.3	977	11	US-11-093-274-39	Sequence 39, Appl
67	61.5	13.3	1145	11	US-11-188-298-16637	Sequence 16637, A
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69	60.5	13.1	106	11	US-11-144-947-341	Sequence 341, App
70	60.5	13.1	463	11	US-11-087-099-7201	Sequence 7201, App
71	60.5	13.1	463	11	US-11-087-099-11335	Sequence 11335, A
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76	60	13.0	525	11	US-11-052-554A-209	Sequence 209, App
77	59	12.8	310	11	US-11-188-298-17559	Sequence 17559, A
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98	58	12.6	394	11	US-11-188-298-926	Sequence 926, App
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117	57	12.4	458	11	US-11-188-298-8947	Sequence 8947, Ap
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135	55.5	12.0	214	9	US-10-993-143-18	Sequence 18, Appl	212	54	11.7	346	11	US-11-186-284-189	Sequence 189, App
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139	55.5	12.0	384	11	US-11-108-185-16	Sequence 16, Appl	216	54	11.7	348	11	US-11-054-281-69	Sequence 69, Appl
140	55.5	12.0	384	11	US-11-108-185-18	Sequence 18, Appl	217	54	11.7	348	11	US-11-054-281-98	Sequence 98, Appl
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143	55.5	12.0	587	11	US-11-172-740-967	Sequence 967, App	220	54	11.7	404	11	US-11-188-298-5135	Sequence 5135, Ap
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151	55	11.9	255	9	US-10-506-454-1677	Sequence 1677, Ap	225	54	11.7	573	11	US-11-087-099-7557	Sequence 7557, Ap
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163	55	11.9	756	11	US-11-188-298-8848	Sequence 8848, Ap	237	53.5	11.6	429	9	US-10-973-115B-94	Sequence 94, Appl
164	55	11.9	786	9	US-10-485-310-10	Sequence 10, Appl	238	53.5	11.6	429	11	US-11-290-153-94	Sequence 94, Appl
165	54.5	11.8	186	11	US-11-044-899-23	Sequence 23, Appl	241	53.5	11.6	429	11	US-11-096-568A-30946	Sequence 30946, A
166	54.5	11.8	189	11	US-11-096-568A-27999	Sequence 27999, A	242	53.5	11.6	482	11	US-11-096-568A-30945	Sequence 30945, A
167	54.5	11.8	189	11	US-11-096-568A-30670	Sequence 30670, A	243	53.5	11.6	485	11	US-11-096-568A-30945	Sequence 5, Appl
168	54.5	11.8	197	11	US-11-096-568A-27998	Sequence 27998, A	244	53.5	11.6	495	9	US-10-613-744-5	Sequence 30944, A
169	54.5	11.8	197	11	US-11-096-568A-30669	Sequence 30669, A	245	53.5	11.6	504	11	US-11-087-099-3671	Sequence 3671, Ap
170	54.5	11.8	239	11	US-11-096-568A-27997	Sequence 27997, A	246	53.5	11.6	593	11	US-11-188-298-14339	Sequence 14339, A
171	54.5	11.8	293	11	US-11-096-568A-27060	Sequence 27060, A	247	53.5	11.6	593	11	US-11-087-099-9040	Sequence 9040, Ap
172	54.5	11.8	294	11	US-11-096-568A-32262	Sequence 32262, A	248	53.5	11.6	594	11	US-11-188-298-8366	Sequence 8366, Ap
173	54.5	11.8	306	11	US-11-096-568A-32261	Sequence 32261, A	249	53.5	11.6	594	11	US-11-145-631-11	Sequence 11, Appl
174	54.5	11.8	308	11	US-11-241-677-14	Sequence 14, Appl	250	53.5	11.6	898	11	US-11-072-512-2538	Sequence 2538, Ap
175	54.5	11.8	340	11	US-11-096-568A-27059	Sequence 27059, A	251	53	11.5	165	11	US-11-087-099-4479	Sequence 4479, Ap
176	54.5	11.8	357	11	US-11-096-568A-32260	Sequence 32260, A	252	53	11.5	170	11	US-11-087-099-4479	Sequence 2, Appl
177	54.5	11.8	364	11	US-11-188-298-4618	Sequence 4618, Ap	253	53	11.5	223	11	US-11-055-822-1130	Sequence 1130, Ap
178	54.5	11.8	369	11	US-11-096-568A-28455	Sequence 28455, A	254	53	11.5	239	11	US-10-995-561-552	Sequence 552, App
179	54.5	11.8	371	11	US-11-096-568A-28454	Sequence 28454, A	255	53	11.5	267	9	US-10-995-561-553	Sequence 553, App
180	54.5	11.8	371	11	US-11-096-568A-29702	Sequence 29702, A	256	53	11.5	301	11	US-11-079-463-6653	Sequence 6653, Ap
181	54.5	11.8	373	11	US-11-096-568A-28453	Sequence 28453, A	257	53	11.5	309	11	US-11-087-099-3288	Sequence 3288, Ap
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183	54.5	11.8	383	11	US-11-096-568A-29700	Sequence 29700, A	259	53	11.5	309	11	US-11-188-298-1836	Sequence 1836, Ap
184	54.5	11.8	384	11	US-11-108-185-2	Sequence 2, Appl	260	53	11.5	376	11	US-11-188-298-4820	Sequence 4820, Ap
185	54.5	11.8	384	11	US-11-108-185-4	Sequence 4, Appl	261	53	11.5	379	11	US-11-087-099-4820	Sequence 17317, A
186	54.5	11.8	384	11	US-11-087-099-9360	Sequence 9360, Ap	262	53	11.5	394	11	US-11-188-298-17317	Sequence 4276, Ap
187	54.5	11.8	394	11	US-11-096-568A-27058	Sequence 27058, A	263	53	11.5	421	11	US-11-188-298-4276	Sequence 2764, Ap
188	54.5	11.8	420	11	US-11-096-568A-23920	Sequence 23920, A	264	53	11.5	469	11	US-11-188-298-384	Sequence 384, Ap
189	54.5	11.8	422	11	US-11-087-099-1523	Sequence 1523, Ap	265	53	11.5	469	11	US-11-188-298-4424	Sequence 4424, Ap
190	54.5	11.8	422	11	US-11-087-099-1957	Sequence 1957, Ap	266	53	11.5	469	11	US-11-188-298-17299	Sequence 17299, A
191	54.5	11.8	424	11	US-11-096-568A-23919	Sequence 23919, A	267	53	11.5	469	11	US-11-188-298-17884	Sequence 17884, A
192	54.5	11.8	425	11	US-11-139-425-4	Sequence 4, Appl	268	53	11.5	603	11	US-11-096-568A-28303	Sequence 28303, A
193	54.5	11.8	622	11	US-11-045-004-780	Sequence 780, App	269	53	11.5	612	11	US-11-120-308-174	Sequence 174, App
194	54.5	11.8	809	11	US-11-188-298-13996	Sequence 13996, Ap	270	53	11.5	701	11	US-11-096-568A-28302	Sequence 28302, A
195	54.5	11.8	895	11	US-11-150-406-2	Sequence 2, Appl	271	53	11.5	701	11	US-11-096-568A-28301	Sequence 28301, A
196	54.5	11.8	920	9	US-10-821-234-1129	Sequence 1129, Ap	272	53	11.5	776	11	US-11-188-298-446	Sequence 446, App
197	54	11.7	55	11	US-11-240-769-80	Sequence 80, Appl	273	53	11.5	776	11	US-11-079-463-9349	Sequence 9349, Ap
198	54	11.7	139	11	US-11-096-568A-14847	Sequence 14847, A	274	52.5	11.4	250	11	US-11-096-568A-15102	Sequence 15102, A
199	54	11.7	143	11	US-11-087-099-767	Sequence 767, App	275	52.5	11.4	292	11	US-11-096-568A-23663	Sequence 23663, A
200	54	11.7	191	11	US-11-096-568A-26954	Sequence 26954, A	276	52.5	11.4	292	11	US-11-096-568A-15101	Sequence 15101, A
201	54	11.7	194	11	US-11-096-568A-14846	Sequence 14846, A	277	52.5	11.4	321	11	US-11-096-568A-23662	Sequence 23662, A
202	54	11.7	237	11	US-11-096-568A-14845	Sequence 14845, A	278	52.5	11.4	321	11	US-11-096-568A-15100	Sequence 15100, A
203	54	11.7	246	11	US-11-096-568A-26953	Sequence 26953, A	279	52.5	11.4	354	11	US-11-096-568A-23661	Sequence 23661, A
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205	54	11.7	253	11	US-11-096-568A-2860	Sequence 2860, Ap	281	52.5	11.4	357	11	US-11-087-099-6761	Sequence 6761, Ap
206	54	11.7	253	11	US-11-096-568A-2862	Sequence 2862, Ap	282	52.5	11.4	377	11	US-11-188-298-17198	Sequence 17198, Ap
207	54	11.7	277	11	US-11-096-568A-26952	Sequence 26952, A	283	52.5	11.4	377	11	US-11-108-185-6	Sequence 6, Appl
208	54	11.7	316	11	US-11-188-298-2012	Sequence 2012, Ap	284	52.5	11.4	384	11	US-11-108-185-8	Sequence 8, Appl
209	54	11.7	316	11	US-11-188-298-16808	Sequence 16808, A	285	52.5	11.4	384	11	US-11-108-185-10	Sequence 10, Appl
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287	52.5	11.4	384	11	US-11-108-185-12	Sequence 12, Appl	390	51.5	11.2	808	11	US-11-072-513-2654	Sequence 2654, Ap
288	52.5	11.4	463	11	US-11-124-3678-374	Sequence 374, App	391	51.5	11.2	1003	11	US-11-188-298-8292	Sequence 8292, Ap
289	52.5	11.4	468	11	US-11-087-099-4740	Sequence 4740, App	392	51.5	11.2	1167	9	US-10-455-772-986	Sequence 986, App
290	52.5	11.4	468	11	US-11-188-298-15353	Sequence 15353, A	393	51.5	11.2	1167	9	US-10-455-772-990	Sequence 990, App
291	52.5	11.4	496	11	US-11-087-099-4813	Sequence 4813, Ap	394	51.5	11.2	1167	9	US-10-455-772-992	Sequence 992, App
292	52.5	11.4	496	11	US-11-188-298-4413	Sequence 4413, Ap	395	51.5	11.2	1204	9	US-10-455-772-988	Sequence 988, App
293	52.5	11.4	612	11	US-11-072-740-1347	Sequence 1347, Ap	396	51.5	11.2	2426	11	US-11-203-806A-11	Sequence 11, Appl
294	52.5	11.4	763	11	US-11-072-512-2766	Sequence 2766, Ap	397	51	11.1	92	11	US-11-174-413-11	Sequence 11, Appl
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296	52	11.3	112	11	US-11-000-463-282	Sequence 282, App	399	51	11.1	135	11	US-11-188-298-4538	Sequence 4538, Ap
297	52	11.3	112	11	US-11-000-463-754	Sequence 754, App	400	51	11.1	198	11	US-11-188-298-2422	Sequence 2422, Ap
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299	52	11.3	151	9	US-10-920-876-3	Sequence 95, Appl	402	51	11.1	247	9	US-10-507-876A-1	Sequence 1, Appl
300	52	11.3	243	9	US-10-511-538-95	Sequence 66, Appl	403	51	11.1	258	11	US-11-096-568A-3312	Sequence 3312, Ap
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302	52	11.3	260	11	US-11-451-455-10	Sequence 22, Appl	405	51	11.1	285	9	US-10-467-657-5894	Sequence 5894, Ap
303	52	11.3	310	11	US-11-010-795-22	Sequence 22, Appl	406	51	11.1	285	9	US-10-467-657-7494	Sequence 7494, Ap
304	52	11.3	359	8	US-10-511-937-2932	Sequence 2932, Ap	407	51	11.1	280	11	US-11-143-980-34	Sequence 34, Appl
305	52	11.3	359	8	US-10-511-937-2955	Sequence 2955, Ap	408	51	11.1	313	11	US-11-096-568A-4270	Sequence 4270, Ap
306	52	11.3	359	11	US-11-152-366-38	Sequence 38, Appl	409	51	11.1	321	9	US-10-329-258-18	Sequence 18, Appl
307	52	11.3	378	11	US-11-082-389-404	Sequence 404, App	410	51	11.1	321	9	US-11-096-568A-4269	Sequence 4269, Ap
308	52	11.3	401	11	US-11-000-365-50	Sequence 50, Appl	411	51	11.1	329	11	US-11-096-568A-3311	Sequence 3311, Ap
309	52	11.3	401	11	US-11-032-794-50	Sequence 50, Appl	412	51	11.1	334	11	US-11-096-568A-3310	Sequence 3310, Ap
310	52	11.3	443	11	US-11-079-463-7888	Sequence 7888, Ap	413	51	11.1	378	11	US-11-188-298-5381	Sequence 5381, Ap
311	52	11.3	444	11	US-11-087-099-1654	Sequence 1654, Ap	414	51	11.1	389	11	US-11-188-298-6171	Sequence 6171, Ap
312	52	11.3	448	11	US-11-188-298-14870	Sequence 14870, A	415	51	11.1	420	11	US-11-188-298-2854	Sequence 2854, Ap
313	52	11.3	450	11	US-11-188-298-19216	Sequence 19216, A	416	51	11.1	420	9	US-10-467-657-790	Sequence 790, App
314	52	11.3	462	11	US-11-087-099-744	Sequence 744, App	417	51	11.1	439	11	US-11-087-099-7449	Sequence 7449, Ap
315	52	11.3	467	11	US-11-087-099-10123	Sequence 10123, A	418	51	11.1	450	11	US-11-045-004-2619	Sequence 2619, Ap
316	52	11.3	467	11	US-11-188-298-20347	Sequence 20347, A	419	51	11.1	452	11	US-11-188-298-4814	Sequence 4814, Ap
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320	52	11.3	628	11	US-11-188-298-4635	Sequence 4635, Ap	423	51	11.1	514	11	US-11-188-298-14827	Sequence 14827, A
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322	52	11.3	711	9	US-10-467-657-2966	Sequence 2966, Ap	425	51	11.1	551	11	US-11-188-298-4086	Sequence 4086, Ap
323	52	11.3	772	11	US-11-188-298-4025	Sequence 4025, Ap	426	51	11.1	553	11	US-11-087-099-1793	Sequence 1793, Ap
324	52	11.3	773	11	US-11-188-298-15538	Sequence 15538, A	427	51	11.1	692	11	US-11-188-298-5840	Sequence 5840, Ap
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340	52	11.3	2138	9	US-10-784-004-639	Sequence 639, App	429	51	11.1	719	8	US-10-505-928-443	Sequence 443, App
341	52	11.3	2221	11	US-11-126-313-30	Sequence 30, Appl	430	51	11.1	749	9	US-10-516-441-2	Sequence 2, Appl
342	51.5	11.2	59	9	US-10-689-742-174	Sequence 174, App	431	51	11.1	774	11	US-11-000-463-459	Sequence 459, App
343	51.5	11.2	112	11	US-11-176-830-614	Sequence 614, App	432	51	11.1	794	11	US-11-087-099-9936	Sequence 9936, Ap
344	51.5	11.2	123	11	US-11-072-512-2234	Sequence 2234, Ap	433	51	11.1	794	11	US-11-188-298-2291	Sequence 2291, Ap
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357	51.5	11.2	211	11	US-11-186-284-22	Sequence 22, Appl	435	51	11.1	967	11	US-10-505-928-795	Sequence 795, App
358	51.5	11.2	212	8	US-10-505-928-298	Sequence 298, App	436	51	11.1	967	11	US-11-054-281-14	Sequence 14, Appl
359	51.5	11.2	212	11	US-11-288-493-68	Sequence 68, Appl	437	51	11.1	967	11	US-11-054-281-74	Sequence 74, Appl
360	51.5	11.2	244	9	US-10-510-386-110	Sequence 110, App	438	51	11.1	967	11	US-11-054-281-75	Sequence 75, Appl
361	51.5	11.2	245	11	US-11-096-568A-10277	Sequence 10277, A	439	51	11.1	1007	11	US-11-051-720-1445	Sequence 1445, Ap
363	51.5	11.2	307	9	US-10-203-486-4	Sequence 4, Appl	440	51	11.1	1305	11	US-11-051-720-1370	Sequence 1370, Ap
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369	51.5	11.2	312	11	US-11-082-389-346	Sequence 346, App	442	51	11.1	1484	8	US-11-176-830-615	Sequence 615, App
370	51.5	11.2	327	11	US-11-096-568A-4231	Sequence 4231, Ap	443	50.5	11.0	112	11	US-11-176-830-615	Sequence 10225, A
371	51.5	11.2	349	11	US-11-096-568A-4230	Sequence 4230, Ap	444	50.5	11.0	124	11	US-11-098-686-10225	Sequence 2706, Ap
372	51.5	11.2	370	11	US-11-045-004-127	Sequence 127, App	445	50.5	11.0	142	11	US-11-072-513-2706	Sequence 66, Appl
373	51.5	11.2	373	11	US-11-086-568A-4229	Sequence 4229, Ap	446	50.5	11.0	207	9	US-10-921-793-66	Sequence 370, App
374	51.5	11.2	380	11	US-11-096-568A-4595	Sequence 4595, Ap	447	50.5	11.0	207	9	US-10-501-035-370	Sequence 66, Appl
375	51.5	11.2	380	11	US-11-087-099-6739	Sequence 6739, Ap	448	50.5	11.0	207	9	US-10-942-042-66	Sequence 66, Appl
376	51.5	11.2	382	11	US-11-124-368A-173	Sequence 173, App	449	50.5	11.0	207	11	US-11-075-400-6	Sequence 97, Appl
377	51.5	11.2	382	11	US-11-124-368A-174	Sequence 174, App	450	50.5	11.0	207	11	US-11-075-400-6	Sequence 97, Appl
378	51.5	11.2	382	11	US-11-127-877-58	Sequence 58, Appl	451	50.5	11.0	207	11	US-11-075-047A-97	Sequence 344, App
379	51.5	11.2	388	11	US-11-096-568A-4594	Sequence 4594, Ap	452	50.5	11.0	249	9	US-10-454-437-344	Sequence 14328, A
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383	51.5	11.2	469	11	US-11-087-099-321	Sequence 321, App	456	50.5	11.0	317	11	US-11-188-298-21152	Sequence 7868, Ap
384	51.5	11.2	469	11	US-11-087-099-6164	Sequence 6164, Ap	457	50.5	11.0	327	11	US-11-188-298-7868	Sequence 9495, Ap
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387	51.5	11.2	537	11	US-11-179-958A-2	Sequence 2, Appl	460	50.5	11.0	379	11	US-11-096-568A-9493	Sequence 282, App
388	51.5	11.2	543	11	US-11-087-099-4195	Sequence 4195, Ap	461	50.5	11.0	469	9	US-10-330-773-292	Sequence 4797, Ap
389	51.5	11.2	766	11	US-11-188-298-9041	Sequence 9041, App	462	50.5	11.0	471	11	US-11-087-099-4797	

463	50.5	11.0	471	11	US-11-087-099-9111	Sequence 9111, Ap	541	50	10.8	512	11	US-11-079-463-9256	Sequence 9256, Ap
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467	50.5	11.0	504	11	US-11-188-298-18441	Sequence 18441, A	545	50	10.8	522	11	US-11-087-099-312	Sequence 312, App
468	50.5	11.0	529	11	US-11-033-039-487	Sequence 487, App	546	50	10.8	569	11	US-11-087-099-3955	Sequence 3955, Ap
469	50.5	11.0	529	11	US-11-155-288-1	Sequence 1, Appli	547	50	10.8	711	11	US-11-188-298-8940	Sequence 8940, Ap
470	50.5	11.0	535	11	US-11-087-099-2008	Sequence 2008, Ap	548	50	10.8	748	9	US-10-516-241-4	Sequence 4, Appli
471	50.5	11.0	542	11	US-11-188-298-1678	Sequence 1678, Ap	549	50	10.8	939	11	US-11-098-686-10121	Sequence 10121, A
472	50.5	11.0	548	11	US-11-096-568A-26941	Sequence 26941, A	550	49.5	10.7	188	9	US-10-506-454-422	Sequence 422, App
473	50.5	11.0	549	11	US-11-096-568A-26940	Sequence 26940, A	551	49.5	10.7	200	9	US-10-498-026-118	Sequence 118, App
474	50.5	11.0	572	11	US-11-043-889-13	Sequence 13, Appli	552	49.5	10.7	204	11	US-11-033-039-271	Sequence 271, App
475	50.5	11.0	694	11	US-11-079-463-6032	Sequence 6032, Ap	553	49.5	10.7	218	11	US-11-045-004-648	Sequence 648, App
476	50.5	11.0	736	11	US-11-087-099-9655	Sequence 9655, Ap	554	49.5	10.7	236	11	US-11-096-568A-4557	Sequence 4557, Ap
477	50.5	11.0	745	11	US-11-087-099-5534	Sequence 5534, Ap	555	49.5	10.7	252	9	US-10-821-234-1445	Sequence 1445, Ap
478	50.5	11.0	771	11	US-11-079-463-7685	Sequence 7685, Ap	556	49.5	10.7	252	9	US-10-986-405-198	Sequence 198, App
479	50.5	11.0	804	9	US-10-330-773-289	Sequence 289, App	557	49.5	10.7	282	11	US-11-186-284-8	Sequence 8, Appli
480	50.5	11.0	974	9	US-10-531-036-35	Sequence 35, Appli	558	49.5	10.7	282	11	US-11-172-610-11	Sequence 11, Appli
481	50.5	11.0	1033	11	US-11-079-463-9280	Sequence 9280, Ap	559	49.5	10.7	262	9	US-10-793-626-1568	Sequence 1568, Ap
482	50.5	11.0	1211	11	US-11-186-284-4	Sequence 4, Appli	560	49.5	10.7	278	11	US-11-188-298-7005	Sequence 7005, Ap
483	50	10.8	82	9	US-10-467-657-4684	Sequence 4684, Ap	561	49.5	10.7	283	9	US-10-506-454-1043	Sequence 1043, Ap
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490	50	10.8	122	11	US-11-188-298-8526	Sequence 8526, Ap	563	49.5	10.7	296	11	US-11-229-769-293	Sequence 293, App
491	50	10.8	128	11	US-11-188-298-10050	Sequence 10050, Ap	564	49.5	10.7	303	11	US-11-188-298-18841	Sequence 18841, A
492	50	10.8	128	11	US-11-188-298-10032	Sequence 10032, Ap	565	49.5	10.7	328	11	US-11-096-568A-4556	Sequence 4556, Ap
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495	50	10.8	146	11	US-11-188-298-21847	Sequence 21847, A	568	49.5	10.7	334	11	US-11-079-463-9185	Sequence 9185, Ap
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497	50	10.8	151	11	US-11-188-298-1808	Sequence 1808, Ap	570	49.5	10.7	380	11	US-11-087-099-4611	Sequence 4611, App
498	50	10.8	151	11	US-11-188-298-7383	Sequence 7383, Ap	571	49.5	10.7	380	11	US-11-087-099-4713	Sequence 4713, Ap
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501	50	10.8	159	11	US-11-188-298-15712	Sequence 15712, A	574	49.5	10.7	414	9	US-10-793-626-806	Sequence 806, App
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504	50	10.8	164	11	US-11-188-298-1570	Sequence 1570, Ap	577	49.5	10.7	470	11	US-11-072-513-3775	Sequence 3775, Ap
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508	50	10.8	189	11	US-11-188-298-7630	Sequence 7630, Ap	581	49.5	10.7	527	11	US-11-188-298-12326	Sequence 12326, A
509	50	10.8	193	11	US-11-188-298-10695	Sequence 10695, A	582	49.5	10.7	557	11	US-11-191-374-4	Sequence 4, Appli
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514	50	10.8	198	11	US-11-188-298-20502	Sequence 20502, A	587	49.5	10.7	628	11	US-11-183-136-12	Sequence 11801, A
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516	50	10.8	202	11	US-11-188-298-6481	Sequence 6481, Ap	589	49.5	10.7	656	11	US-11-079-463-7923	Sequence 350, App
517	50	10.8	243	11	US-11-188-298-22084	Sequence 22084, A	591	49.5	10.7	660	11	US-10-973-1158-350	Sequence 10456, A
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521	50	10.8	339	11	US-11-188-298-7093	Sequence 7093, Ap	597	49.5	10.7	785	11	US-11-087-099-9941	Sequence 8676, Ap
522	50	10.8	341	11	US-11-096-568A-16888	Sequence 16888, A	598	49.5	10.7	960	11	US-11-087-099-8676	Sequence 283, App
523	50	10.8	346	11	US-11-000-365-52	Sequence 52, Appli	599	49.5	10.7	1461	11	US-11-052-554A-283	Sequence 67, Appli
524	50	10.8	346	11	US-11-032-794-52	Sequence 52, Appli	600	49	10.6	92	11	US-11-174-413-67	Sequence 63, Appli
525	50	10.8	348	11	US-11-087-099-3175	Sequence 175, Ap	601	49	10.6	167	11	US-11-103-957-63	Sequence 8173, Ap
526	50	10.8	351	11	US-11-054-281-100	Sequence 100, App	602	49	10.6	188	11	US-11-079-463-8373	Sequence 1465, Ap
527	50	10.8	374	11	US-11-188-298-14269	Sequence 14269, A	603	49	10.6	203	11	US-11-096-568A-1465	Sequence 4799, Ap
528	50	10.8	388	11	US-11-188-298-11099	Sequence 11099, A	604	49	10.6	225	11	US-11-087-099-4799	Sequence 4799, Ap
529	50	10.8	390	9	US-10-793-626-1422	Sequence 1422, Ap	605	49	10.6	239	11	US-11-136-341A-3	Sequence 3, Appli
530	50	10.8	391	11	US-11-207-626A-16	Sequence 16, Appli	606	49	10.6	284	11	US-11-096-568A-31683	Sequence 31683, A
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533	50	10.8	449	11	US-11-087-099-1645	Sequence 1645, Ap	609	49	10.6	276	9	US-10-467-657-4158	Sequence 54, App
534	50	10.8	449	11	US-11-188-298-1633	Sequence 1633, Ap	610	49	10.6	304	9	US-10-515-002-249	Sequence 24, App
535	50	10.8	457	9	US-10-982-545-13	Sequence 8, Appli	611	49	10.6	318	11	US-11-146-428-54	Sequence 20415, A
536	50	10.8	457	9	US-10-982-545-13	Sequence 13, Appli	612	49	10.6	320	11	US-11-188-298-12687	Sequence 12687, A
537	50	10.8	469	11	US-11-188-298-16378	Sequence 16378, A	613	49	10.6	335	11	US-11-188-298-20879	Sequence 20879, A
538	50	10.8	477	11	US-11-087-099-1186	Sequence 1186, Ap	614	49	10.6	335	11	US-11-183-664-2	Sequence 2, Appli
539	50	10.8	480	11	US-11-188-298-6789	Sequence 6789, Ap	615	49	10.6	335	11	US-11-183-664-2	Sequence 20135, A
540	50	10.8	483	11	US-11-087-099-11681	Sequence 11681, A	616	49	10.6	335	11	US-11-188-298-20135	Sequence 20135, A



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622	49	10.6	352	11	US-11-127-877-61	Sequence 61, App	698	48.5	10.5	112	11	US-11-176-830-623	Sequence 623, App
623	49	10.6	352	11	US-11-188-298-19581	Sequence 19581, A	699	48.5	10.5	112	11	US-11-176-830-624	Sequence 624, App
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625	49	10.6	361	11	US-11-096-568A-34442	Sequence 34442, A	701	48.5	10.5	112	11	US-11-176-830-626	Sequence 626, App
626	49	10.6	369	11	US-11-096-568A-34441	Sequence 34441, A	702	48.5	10.5	112	11	US-11-176-830-627	Sequence 627, App
627	49	10.6	374	11	US-11-087-099-4538	Sequence 4538, App	703	48.5	10.5	112	11	US-11-176-830-628	Sequence 628, App
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630	49	10.6	399	11	US-11-087-099-10646	Sequence 10646, A	706	48.5	10.5	113	11	US-11-149-309-32	Sequence 32, App
631	49	10.6	417	9	US-10-485-517-419	Sequence 419, App	707	48.5	10.5	113	11	US-11-155-843-124	Sequence 124, App
632	49	10.6	417	11	US-11-188-298-8031	Sequence 8031, App	708	48.5	10.5	132	11	US-11-149-309-31	Sequence 31, App
633	49	10.6	421	11	US-11-096-568A-31682	Sequence 31682, A	709	48.5	10.5	136	11	US-11-155-843-178	Sequence 178, App
634	49	10.6	431	11	US-11-087-099-4831	Sequence 4831, App	710	48.5	10.5	136	11	US-10-511-937-2477	Sequence 2477, App
635	49	10.6	440	11	US-11-096-568A-31681	Sequence 31681, A	711	48.5	10.5	146	8	US-10-511-937-2477	Sequence 2477, App
636	49	10.6	458	11	US-11-087-099-1138	Sequence 1138, App	712	48.5	10.5	146	11	US-11-061-821-42	Sequence 42, App
637	49	10.6	458	11	US-11-087-099-9665	Sequence 9665, App	713	48.5	10.5	157	11	US-11-051-267-27	Sequence 27, App
638	49	10.6	458	11	US-11-188-298-19977	Sequence 19977, A	714	48.5	10.5	201	11	US-11-096-568A-25909	Sequence 25909, A
639	49	10.6	458	11	US-11-045-004-1603	Sequence 1603, App	715	48.5	10.5	212	11	US-11-096-568A-6662	Sequence 6662, App
640	49	10.6	459	11	US-11-087-099-9041	Sequence 9041, App	716	48.5	10.5	219	11	US-11-096-568A-6661	Sequence 6661, App
641	49	10.6	468	11	US-11-167-273-1	Sequence 1, App	717	48.5	10.5	220	11	US-11-096-568A-25908	Sequence 25908, A
642	49	10.6	469	11	US-11-188-298-7196	Sequence 7196, App	718	48.5	10.5	234	11	US-11-096-568A-25907	Sequence 25907, A
643	49	10.6	469	11	US-11-188-298-11220	Sequence 11220, A	719	48.5	10.5	250	11	US-11-096-568A-6660	Sequence 6660, App
644	49	10.6	469	11	US-11-188-298-15611	Sequence 15611, A	720	48.5	10.5	264	11	US-11-188-298-15584	Sequence 15584, A
645	49	10.6	470	11	US-11-188-298-21250	Sequence 21250, A	721	48.5	10.5	284	9	US-10-821-234-1280	Sequence 1280, App
646	49	10.6	476	11	US-11-188-298-15047	Sequence 15047, A	722	48.5	10.5	289	8	US-10-505-928-375	Sequence 375, App
647	49	10.6	479	11	US-11-188-298-15602	Sequence 15602, A	723	48.5	10.5	293	11	US-11-096-568A-19465	Sequence 19465, A
648	49	10.6	493	11	US-11-096-568A-18222	Sequence 18222, A	724	48.5	10.5	297	11	US-11-096-568A-19464	Sequence 19464, A
649	49	10.6	493	11	US-11-045-004-49	Sequence 49, App	725	48.5	10.5	297	11	US-11-096-568A-33735	Sequence 33735, A
650	49	10.6	495	8	US-10-511-937-2971	Sequence 2971, App	726	48.5	10.5	300	11	US-11-079-463-8196	Sequence 8196, App
651	49	10.6	496	11	US-11-096-568A-18221	Sequence 18221, App	727	48.5	10.5	306	11	US-11-188-298-15809	Sequence 15809, App
652	49	10.6	500	11	US-11-072-512-3456	Sequence 3456, App	728	48.5	10.5	311	11	US-11-087-099-1905	Sequence 1905, App
653	49	10.6	509	9	US-10-821-234-1168	Sequence 1168, App	729	48.5	10.5	312	11	US-11-188-298-20208	Sequence 20208, A
654	49	10.6	509	11	US-11-096-568A-26580	Sequence 26580, A	730	48.5	10.5	312	11	US-11-096-568A-19463	Sequence 19463, A
655	49	10.6	509	11	US-11-188-298-9974	Sequence 9974, App	731	48.5	10.5	336	11	US-11-188-298-7794	Sequence 7794, App
656	49	10.6	519	11	US-11-188-298-12160	Sequence 12160, A	732	48.5	10.5	337	11	US-11-188-298-17347	Sequence 17347, App
657	49	10.6	622	11	US-11-188-298-19008	Sequence 19008, A	733	48.5	10.5	337	11	US-11-096-568A-28543	Sequence 28543, A
658	49	10.6	648	11	US-11-188-298-16751	Sequence 16751, A	734	48.5	10.5	340	11	US-11-096-568A-28542	Sequence 28542, A
659	49	10.6	689	11	US-11-188-298-16751	Sequence 16751, A	735	48.5	10.5	355	11	US-11-087-099-12235	Sequence 12235, A
660	49	10.6	690	11	US-11-079-463-6647	Sequence 6647, App	736	48.5	10.5	362	11	US-11-079-463-8992	Sequence 8992, App
661	49	10.6	735	9	US-10-506-434A-75	Sequence 75, App	737	48.5	10.5	374	11	US-11-045-004-318	Sequence 318, App
662	49	10.6	740	11	US-11-124-367A-293	Sequence 293, App	738	48.5	10.5	400	11	US-11-072-512-3621	Sequence 3621, App
663	49	10.6	760	11	US-11-124-367A-292	Sequence 292, App	739	48.5	10.5	404	11	US-11-254-173-56	Sequence 56, App
664	49	10.6	768	11	US-11-079-463-10296	Sequence 10296, A	740	48.5	10.5	442	10	US-11-264-784-9	Sequence 9, App
665	49	10.6	773	11	US-11-188-298-20543	Sequence 20543, A	741	48.5	10.5	462	11	US-11-188-298-8905	Sequence 8905, App
666	49	10.6	790	11	US-11-188-298-7469	Sequence 7469, App	742	48.5	10.5	485	11	US-11-087-099-9429	Sequence 9429, App
667	49	10.6	826	11	US-11-087-099-6618	Sequence 6618, App	743	48.5	10.5	485	11	US-11-188-298-19761	Sequence 19761, A
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670	49	10.6	914	11	US-11-148-108-41	Sequence 1066, App	746	48.5	10.5	505	9	US-10-467-657-240	Sequence 240, App
671	49	10.6	914	11	US-11-264-096-2054	Sequence 2054, App	747	48.5	10.5	510	11	US-11-188-298-13840	Sequence 13840, A
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675	49	10.6	1023	11	US-10-230-153-200	Sequence 200, App	751	48.5	10.5	528	11	US-11-188-298-3223	Sequence 3223, App
676	49	10.6	1070	9	US-10-537-002-14	Sequence 14, App	752	48.5	10.5	533	9	US-10-467-657-8	Sequence 8, App
677	49	10.6	1073	9	US-10-537-002-11	Sequence 11, App	753	48.5	10.5	561	11	US-11-096-568A-6968	Sequence 6968, App
678	49	10.6	1197	11	US-11-087-099-8238	Sequence 8238, App	754	48.5	10.5	567	9	US-10-467-657-4328	Sequence 4328, App
679	49	10.6	1197	11	US-11-122-396-7	Sequence 7, App	755	48.5	10.5	608	9	US-10-873-528-8	Sequence 8, App
680	49	10.6	1197	11	US-10-207-797-162	Sequence 162, App	756	48.5	10.5	608	11	US-11-087-099-3204	Sequence 3204, App
681	49	10.6	1197	11	US-11-176-830-209	Sequence 209, App	757	48.5	10.5	610	11	US-11-045-004-1527	Sequence 1527, App
682	49	10.6	1197	11	US-11-176-830-603	Sequence 603, App	758	48.5	10.5	610	11	US-11-045-004-1527	Sequence 1527, App
683	48.5	10.5	57	9	US-10-207-797-162	Sequence 162, App	759	48.5	10.5	615	9	US-10-982-545-14	Sequence 14, App
684	48.5	10.5	112	11	US-11-176-830-603	Sequence 603, App	760	48.5	10.5	616	9	US-10-982-545-5	Sequence 5, App
685	48.5	10.5	112	11	US-11-176-830-604	Sequence 604, App	761	48.5	10.5	616	9	US-10-501-035-384	Sequence 384, App
686	48.5	10.5	112	11	US-11-176-830-607	Sequence 607, App	762	48.5	10.5	638	11	US-11-188-298-2271	Sequence 2271, App
687	48.5	10.5	112	11	US-11-176-830-609	Sequence 609, App	763	48.5	10.5	638	11	US-11-188-298-14582	Sequence 14582, A
688	48.5	10.5	112	11	US-11-176-830-610	Sequence 610, App	764	48.5	10.5	638	11	US-11-188-298-18598	Sequence 18598, A
689	48.5	10.5	112	11	US-11-176-830-611	Sequence 611, App	765	48.5	10.5	658	11	US-11-188-298-4461	Sequence 4461, App
690	48.5	10.5	112	11	US-11-176-830-616	Sequence 616, App							
691	48.5	10.5	112	11	US-11-176-830-617	Sequence 617, App							
692	48.5	10.5	112	11	US-11-176-830-617	Sequence 617, App							

766	48.5	10.5	658	11	US-11-188-298-18470	Sequence 18470, A	844	48	10.4	713	8	US-10-505-928-345	Sequence 345, App
767	48.5	10.5	687	11	US-11-096-568A-6967	Sequence 6967, App	845	48	10.4	729	11	US-11-087-099-5269	Sequence 5269, App
768	48.5	10.5	702	11	US-11-096-568A-29016	Sequence 29016, A	846	48	10.4	840	9	US-10-645-441-1	Sequence 1, Appl
769	48.5	10.5	707	11	US-11-096-568A-6966	Sequence 6966, App	847	48	10.4	840	9	US-10-725-475-16	Sequence 16, Appl
770	48.5	10.5	749	11	US-11-096-568A-29015	Sequence 29015, A	848	48	10.4	865	11	US-11-188-298-1519	Sequence 1519, App
771	48.5	10.5	764	11	US-11-188-298-8892	Sequence 8892, App	849	48	10.4	869	11	US-11-043-752-45	Sequence 45, Appl
772	48.5	10.5	773	11	US-11-010-239-63	Sequence 63, Appl	850	48	10.4	922	9	US-10-517-939-38	Sequence 38, Appl
773	48.5	10.5	778	9	US-10-505-263-81	Sequence 81, Appl	851	48	10.4	929	11	US-11-087-099-6648	Sequence 6648, App
774	48.5	10.5	789	9	US-10-506-454-597	Sequence 597, App	852	48	10.4	929	11	US-11-087-099-7898	Sequence 7898, App
775	48.5	10.5	893	11	US-10-506-454-597	Sequence 597, App	853	48	10.4	948	9	US-10-485-517-131	Sequence 131, App
776	48.5	10.5	912	9	US-10-964-313-12	Sequence 12, Appl	854	48	10.4	959	11	US-11-188-298-12621	Sequence 12621, A
777	48.5	10.5	1954	9	US-10-784-004-1235	Sequence 1235, App	855	48	10.4	1024	9	US-10-455-772-788	Sequence 788, App
778	48.5	10.5	2589	11	US-11-216-660-9	Sequence 9, Appl	856	48	10.4	1024	9	US-10-455-772-788	Sequence 788, App
779	48	10.4	37	9	US-10-219-783-9	Sequence 9, Appl	857	48	10.4	1071	11	US-11-043-752-44	Sequence 44, Appl
780	48	10.4	68	9	US-10-467-657-4718	Sequence 4718, App	858	48	10.4	1320	11	US-11-188-298-19369	Sequence 19369, A
781	48	10.4	73	11	US-11-229-769-300	Sequence 300, App	859	48	10.4	1322	11	US-11-188-298-17779	Sequence 17779, A
782	48	10.4	74	11	US-11-229-769-229	Sequence 229, App	860	48	10.4	1478	11	US-11-188-298-6040	Sequence 6040, App
783	48	10.4	100	11	US-11-172-740-651	Sequence 651, App	861	48	10.4	1478	11	US-11-188-298-8632	Sequence 8632, App
784	48	10.4	104	11	US-11-188-298-20223	Sequence 20223, A	862	48	10.4	1478	11	US-11-188-298-13053	Sequence 13053, A
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786	48	10.4	210	11	US-11-087-099-4617	Sequence 4617, App	864	48	10.4	1908	9	US-10-915-002-314	Sequence 314, App
787	48	10.4	212	9	US-10-506-454-635	Sequence 635, App	865	48	10.4	2556	11	US-11-050-346-67	Sequence 67, App
788	48	10.4	215	9	US-10-506-454-635	Sequence 635, App	866	47.5	10.3	89	11	US-11-123-896-245	Sequence 245, App
789	48	10.4	220	11	US-11-096-568A-17652	Sequence 17652, A	867	47.5	10.3	94	11	US-11-096-568A-25178	Sequence 25178, A
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791	48	10.4	238	11	US-11-096-568A-17651	Sequence 17651, A	869	47.5	10.3	112	11	US-11-176-830-608	Sequence 608, App
792	48	10.4	238	11	US-11-087-099-4282	Sequence 4282, App	870	47.5	10.3	132	7	US-09-395-493-42	Sequence 42, Appl
793	48	10.4	241	11	US-11-188-298-21854	Sequence 21854, A	871	47.5	10.3	134	11	US-11-096-568A-25177	Sequence 25177, A
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795	48	10.4	254	11	US-11-067-323-460	Sequence 460, App	873	47.5	10.3	205	11	US-11-096-568A-20850	Sequence 20850, A
796	48	10.4	259	11	US-11-072-512-3858	Sequence 3858, App	874	47.5	10.3	209	11	US-11-045-004-1819	Sequence 1819, App
797	48	10.4	271	11	US-11-239-444-2	Sequence 2, Appl	875	47.5	10.3	212	11	US-11-096-568A-6211	Sequence 6211, App
798	48	10.4	285	11	US-11-188-298-7544	Sequence 7544, App	876	47.5	10.3	215	9	US-10-506-454-623	Sequence 623, App
799	48	10.4	308	11	US-11-096-568A-9632	Sequence 9632, App	877	47.5	10.3	230	11	US-11-096-568A-33024	Sequence 33024, A
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801	48	10.4	317	11	US-11-096-568A-2578	Sequence 2578, App	879	47.5	10.3	243	11	US-11-096-568A-8143	Sequence 8143, App
802	48	10.4	325	11	US-11-045-004-1945	Sequence 1945, App	880	47.5	10.3	245	11	US-11-096-568A-6210	Sequence 6210, App
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810	48	10.4	407	11	US-11-092-140-4	Sequence 4, Appl	888	47.5	10.3	288	11	US-11-096-568A-8142	Sequence 8142, App
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812	48	10.4	453	11	US-11-087-099-6300	Sequence 6300, App	890	47.5	10.3	301	11	US-11-079-463-6474	Sequence 6474, App
813	48	10.4	464	11	US-11-087-099-449	Sequence 449, App	891	47.5	10.3	309	11	US-11-188-298-11429	Sequence 11429, A
814	48	10.4	477	11	US-11-188-298-8851	Sequence 8851, App	892	47.5	10.3	313	11	US-11-096-568A-8035	Sequence 8035, App
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816	48	10.4	499	11	US-11-188-298-519	Sequence 20979, App	894	47.5	10.3	325	11	US-11-096-568A-29197	Sequence 29197, A
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818	48	10.4	507	11	US-11-087-099-4463	Sequence 4463, App	896	47.5	10.3	334	11	US-11-096-568A-29078	Sequence 29078, A
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820	48	10.4	508	11	US-11-087-099-6849	Sequence 6849, App	898	47.5	10.3	339	11	US-11-096-568A-23196	Sequence 23196, A
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825	48	10.4	519	11	US-11-079-463-8130	Sequence 8130, App	903	47.5	10.3	367	11	US-11-188-298-2231	Sequence 2231, App
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830	48	10.4	573	11	US-11-188-298-8148	Sequence 8148, App	908	47.5	10.3	383	11	US-11-096-568A-8034	Sequence 8034, App
831	48	10.4	573	11	US-11-188-298-9722	Sequence 9722, App	909	47.5	10.3	385	11	US-11-188-298-11164	Sequence 11164, A
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833	48	10.4	601	11	US-11-072-512-2034	Sequence 2034, App	911	47.5	10.3	387	11	US-11-087-099-2534	Sequence 2534, App
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835	48	10.4	619	11	US-11-096-568A-2576	Sequence 2576, App	913	47.5	10.3	396	11	US-11-087-099-8866	Sequence 8866, App
836	48	10.4	689	11	US-11-045-004-545	Sequence 545, App	914	47.5	10.3	396	11	US-11-087-099-10947	Sequence 10947, A
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918	47.5	10.3	442	11	US-11-096-568A-19021	Sequence 19021, A	1010	47	10.2	254	11	US-11-067-323-272	Sequence 272, App
919	47.5	10.3	455	11	US-11-096-568A-19020	Sequence 19020, A	1011	47	10.2	254	11	US-11-067-323-278	Sequence 278, App
920	47.5	10.3	456	11	US-11-188-298-2769	Sequence 2769, App	1012	47	10.2	254	11	US-11-067-323-282	Sequence 282, App
921	47.5	10.3	466	11	US-11-087-099-10294	Sequence 10294, A	1013	47	10.2	254	11	US-11-067-323-286	Sequence 286, App
922	47.5	10.3	479	11	US-11-098-686-10838	Sequence 10838, A	1014	47	10.2	254	11	US-11-067-323-292	Sequence 292, App
923	47.5	10.3	481	11	US-11-188-298-13506	Sequence 13506, A	1015	47	10.2	254	11	US-11-067-323-294	Sequence 294, App
924	47.5	10.3	485	11	US-11-074-176-10	Sequence 10, App	1016	47	10.2	254	11	US-11-067-323-296	Sequence 296, App
925	47.5	10.3	491	9	US-10-506-454-1574	Sequence 1574, App	1017	47	10.2	254	11	US-11-067-323-304	Sequence 304, App
926	47.5	10.3	491	11	US-11-087-099-6597	Sequence 6597, App	1018	47	10.2	254	11	US-11-067-323-306	Sequence 306, App
927	47.5	10.3	498	11	US-11-188-298-5913	Sequence 5913, App	1019	47	10.2	254	11	US-11-067-323-316	Sequence 316, App
928	47.5	10.3	498	11	US-11-188-298-8627	Sequence 8627, App	1020	47	10.2	254	11	US-11-067-323-326	Sequence 326, App
929	47.5	10.3	508	11	US-11-096-568A-15743	Sequence 15743, A	1021	47	10.2	254	11	US-11-067-323-328	Sequence 328, App
930	47.5	10.3	511	11	US-11-188-298-1881	Sequence 1881, App	1022	47	10.2	254	11	US-11-067-323-330	Sequence 330, App
931	47.5	10.3	518	11	US-11-188-298-9414	Sequence 9414, App	1023	47	10.2	254	11	US-11-067-323-344	Sequence 344, App
933	47.5	10.3	537	11	US-11-096-568A-15742	Sequence 15742, A	1024	47	10.2	254	11	US-11-067-323-352	Sequence 352, App
946	47.5	10.3	537	11	US-11-096-568A-15742	Sequence 15742, A	1025	47	10.2	254	11	US-11-067-323-354	Sequence 354, App
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948	47.5	10.3	572	8	US-10-505-928-98	Sequence 98, App	1027	47	10.2	254	11	US-11-067-323-364	Sequence 364, App
949	47.5	10.3	572	10	US-11-301-554-1815	Sequence 1815, App	1028	47	10.2	254	11	US-11-067-323-370	Sequence 370, App
955	47.5	10.3	584	11	US-11-172-740-969	Sequence 969, App	1029	47	10.2	254	11	US-11-067-323-376	Sequence 376, App
956	47.5	10.3	613	11	US-11-188-298-18016	Sequence 18016, A	1030	47	10.2	254	11	US-11-067-323-378	Sequence 378, App
957	47.5	10.3	623	11	US-11-188-298-16877	Sequence 16877, A	1031	47	10.2	254	11	US-11-067-323-400	Sequence 400, App
958	47.5	10.3	738	8	US-10-511-937-2418	Sequence 2418, App	1032	47	10.2	254	11	US-11-067-323-406	Sequence 406, App
959	47.5	10.3	738	9	US-10-995-561-692	Sequence 692, App	1033	47	10.2	254	11	US-11-067-323-406	Sequence 406, App
960	47.5	10.3	738	9	US-10-995-561-693	Sequence 693, App	1034	47	10.2	257	9	US-10-793-626-3244	Sequence 3244, App
961	47.5	10.3	896	9	US-10-467-657-7004	Sequence 7004, App	1035	47	10.2	263	11	US-11-096-568A-12639	Sequence 12639, A
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963	47	10.2	37	9	US-10-219-783-8	Sequence 8, App	1037	47	10.2	283	9	US-10-454-437-20	Sequence 20, App
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965	47	10.2	116	11	US-11-188-298-743	Sequence 743, App	1039	47	10.2	299	11	US-11-096-568A-12638	Sequence 12638, A
966	47	10.2	122	11	US-11-087-099-6151	Sequence 6151, App	1040	47	10.2	304	11	US-11-188-298-1358	Sequence 1358, App
967	47	10.2	124	11	US-11-096-568A-5220	Sequence 5220, App	1041	47	10.2	304	11	US-10-511-538-168	Sequence 168, App
968	47	10.2	128	11	US-11-188-298-3664	Sequence 3664, App	1042	47	10.2	323	11	US-11-190-188-20	Sequence 20, App
969	47	10.2	130	11	US-11-188-298-10381	Sequence 10381, A	1043	47	10.2	323	11	US-11-096-568A-12637	Sequence 12637, A
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971	47	10.2	142	11	US-11-096-568A-7512	Sequence 7512, App	1045	47	10.2	328	9	US-10-485-517-340	Sequence 340, App
972	47	10.2	142	11	US-11-188-298-6519	Sequence 6519, App	1046	47	10.2	334	11	US-11-188-298-1012	Sequence 1012, App
973	47	10.2	150	11	US-11-188-298-17418	Sequence 17418, A	1047	47	10.2	337	11	US-11-087-099-4299	Sequence 4299, App
974	47	10.2	151	11	US-11-188-298-3618	Sequence 3618, App	1048	47	10.2	337	11	US-11-096-568A-19234	Sequence 19234, A
975	47	10.2	172	11	US-11-087-099-496	Sequence 496, App	1049	47	10.2	338	11	US-11-188-298-1422	Sequence 1422, App
976	47	10.2	174	11	US-11-188-298-9479	Sequence 9479, App	1050	47	10.2	342	11	US-11-188-298-16432	Sequence 16432, App
977	47	10.2	179	11	US-11-096-568A-5219	Sequence 5219, App	1051	47	10.2	345	11	US-11-087-099-8494	Sequence 8494, App
978	47	10.2	187	11	US-11-188-298-18749	Sequence 18749, App	1052	47	10.2	348	11	US-11-188-298-10154	Sequence 10154, A
979	47	10.2	188	11	US-11-188-298-3504	Sequence 3504, App	1053	47	10.2	348	11	US-11-188-298-17115	Sequence 17115, A
980	47	10.2	188	11	US-11-188-298-1626	Sequence 1626, App	1054	47	10.2	358	10	US-11-024-544A-136	Sequence 136, App
981	47	10.2	194	11	US-11-044-899-26	Sequence 26, App	1055	47	10.2	358	10	US-11-024-545-54	Sequence 54, App
982	47	10.2	196	11	US-11-188-298-11507	Sequence 11507, A	1056	47	10.2	358	10	US-11-190-750-109	Sequence 109, App
983	47	10.2	196	11	US-11-188-298-12935	Sequence 12935, A	1057	47	10.2	358	10	US-11-251-466-28	Sequence 28, App
984	47	10.2	197	11	US-11-188-298-13788	Sequence 13788, A	1058	47	10.2	358	10	US-11-254-173-44	Sequence 44, App
985	47	10.2	197	11	US-11-188-298-14635	Sequence 14635, A	1059	47	10.2	358	10	US-11-254-173-44	Sequence 112, App
986	47	10.2	197	11	US-11-188-298-20387	Sequence 20387, A	1060	47	10.2	358	11	US-11-146-428-112	Sequence 12915, A
987	47	10.2	199	11	US-11-188-298-17527	Sequence 17527, A	1061	47	10.2	360	11	US-11-188-298-12915	Sequence 868, App
988	47	10.2	199	11	US-11-188-298-19685	Sequence 19685, A	1062	47	10.2	364	11	US-11-096-568A-19233	Sequence 19233, A
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991	47	10.2	200	11	US-11-188-298-8561	Sequence 8561, App	1065	47	10.2	377	11	US-11-264-096-1949	Sequence 1949, App
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1282	46	10.0	128	11	US-11-264-096-1575	Sequence 1575, Ap	1360	46	10.0	304	9	US-10-846-172A-5	Sequence 5, Appl
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1458	46	10.0	676	11	US-11-188-298-5921	Sequence 5921, Ap							
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1461	46	10.0	756	9	US-10-055-877-188	Sequence 188, Appl							
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Searched: 283416 seqs, 96216763 residues

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Maximum Match 100%

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1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	256.5	55.6	87	2 I59391	transmembrane prot
2	241.5	52.4	88	2 S61552	mammary tumor prot
3	214.5	46.5	87	2 A55571	chloride conductan
4	126.5	27.4	92	2 A40533	CAMP-dependent pro
5	96.5	20.9	58	2 D46435	Na+/K+-exchanging
6	94.5	20.5	53	2 A46435	Na+/K+-exchanging
7	75.5	16.4	58	2 C46435	Na+/K+-exchanging
8	73.5	15.9	58	2 A61088	plastoquinol-plast
9	72	15.6	160	1 A61088	conserved hypotet
10	71	15.4	529	2 F69889	probable membrane
11	69	15.0	150	2 AH0371	hypothetical prote
12	67.5	14.6	135	2 A05009	chorismate synthas
13	66.5	14.4	359	2 B86620	chorismate synthas
14	66.5	14.4	359	2 A72004	potassium channel
15	66.5	14.4	523	2 A38101	potassium channel
16	66	14.3	446	2 B90463	proline/betaine tr
17	64	13.9	525	2 A43531	potassium channel
18	63.5	13.8	309	2 AC1697	probable transport
19	63.5	13.8	309	2 A11325	probable transport
20	63.5	13.8	511	2 A46020	potassium channel
21	63.5	13.8	511	2 S07095	potassium channel
22	63.5	13.8	585	2 A39395	delayed rectifier
23	63.5	13.8	620	2 A70525	hypothetical prote
24	63	13.7	468	2 C96818	hypothetical prote
25	62.5	13.6	299	2 A38111	transcription regu
26	62.5	13.6	679	2 A42073	Shaw type potassi
27	62.5	13.6	769	2 I56546	potassium channel
28	62.5	13.6	910	2 F81974	leucine-tRNA ligas
29	62	13.4	381	2 AB2907	GGDEF family prote

30	62	13.4	393	2 B97682	ggdef family prote
31	62	13.4	589	2 T43295	uracil transport p
32	62	13.4	777	2 S30271	pyocin AP41 large
33	61.5	13.3	342	2 S75086	iron-stress chloro
34	61.5	13.3	433	2 B72025	flagellum-specific
35	61.5	13.3	433	2 A81513	virulence Afraze,
36	61.5	13.3	433	2 H86597	flagellum-specific
37	61.5	13.3	445	2 AD0962	DsdX permease (imp
38	61.5	13.3	990	2 JC8058	laeverin - human
39	61.5	13.3	1499	2 AC2555	hypothetical prote
40	61	13.2	268	2 C87235	conserved hypotet
41	61	13.2	355	2 I51157	major histocompati
42	61	13.2	461	2 B90984	O antigen flippase
43	61	13.2	463	2 A75151	damage-inducible p
44	61	13.2	463	2 B85829	O antigen flippase
45	61	13.2	463	2 G71191	probable DNA damag
46	61	13.2	520	2 D84471	probable membrane
47	60.5	13.1	295	2 C84830	probable protein k
48	60.5	13.1	312	2 B83749	sugar transport sy
49	60.5	13.1	326	2 C90272	hypothetical prote
50	60.5	13.1	354	2 G86276	hypothetical prote
51	60.5	13.1	427	2 B87669	conserved hypotet
52	60.5	13.1	463	2 A10388	probable proline-s
53	60.5	13.1	516	2 T47509	probable transport
54	60.5	13.1	581	2 S17150	potassium channel
55	60.5	13.1	613	2 A39402	potassium channel
56	60.5	13.1	624	2 S22703	voltage-gated pota
57	60.5	13.1	728	2 B81370	phosphoribosylform
58	60	13.0	71	2 C23876	vitellogenin B1 pr
59	60	13.0	208	2 S36155	paired box protein
60	60	13.0	269	2 AH1970	type 4 prelin pe
61	60	13.0	342	2 S57652	transcription fact
62	60	13.0	412	2 A83461	hypothetical prote
63	60	13.0	497	1 WMBELM	membrane protein L
64	60	13.0	538	2 A51175	hypothetical 60.6
65	60	13.0	5232	2 A45086	HC-toxin synthetas
66	59.5	12.9	267	2 G86782	phosphomethylpyrim
67	59.5	12.9	298	2 A82387	amino acid ABC tra
68	59.5	12.9	356	2 T30361	occlusion-derived
69	59.5	12.9	527	2 A48076	glucose transporte
70	59.5	12.9	527	2 A45611	probable hexose tr
71	59	12.8	130	2 B85808	unknown protein en
72	59	12.8	175	2 T11087	NADH2 dehydrogenas
73	59	12.8	177	2 AH1669	probable NAD(P)H o
74	59	12.8	215	2 B85704	probable channel p
75	59	12.8	215	2 F90846	probable channel p
76	59	12.8	215	2 E84871	probable membrane
77	59	12.8	310	2 G87624	integral membrane
78	59	12.8	326	2 AB3607	3-oxoacyl-(acyl-ca
79	59	12.8	419	2 E90446	permease (imported
80	59	12.8	420	2 G96002	probable sugar upt
81	59	12.8	479	2 C95366	NADH2 dehydrogenas
82	59	12.8	558	2 A81599	glycerol 3 phospho
83	59	12.8	653	2 A39922	potassium channel
84	59	12.8	654	2 S11049	potassium channel
85	59	12.8	660	2 S24125	potassium channel
86	59	12.8	802	2 JH0595	potassium channel
87	59	12.8	853	1 CHRTD1	potassium channel
88	59	12.8	857	2 I56529	potassium channel
89	59	12.8	858	2 S31761	potassium channel
90	58.5	12.7	182	2 C83600	hypothetical prote
91	58.5	12.7	384	2 A12962	cellulose synthesi
92	58.5	12.7	389	2 E98320	hypothetical prote
93	58.5	12.7	411	2 H75376	hypothetical prote
94	58.5	12.7	425	2 T50355	hypothetical prote
95	58.5	12.7	463	2 D87201	conserved hypotet
96	58.5	12.7	633	2 E86271	protein F16A1.4
97	58.5	12.7	876	2 G81029	leucine-tRNA ligas
98	58.5	12.7	1095	2 E96744	probable oligopept
99	58.5	12.7	1189	2 I39711	celE protein - Agr
100	58.5	12.7	2712	2 T30949	hypothetical prote
101	58.5	12.7	3864	2 D87757	protein C4AE4.1a
102	58	12.6	114	2 F69782	hypothetical prote

103	58	12.6	185	2	AG1054	probable exported	176	56	12.1	594	2	A83096	probable permealase
104	58	12.6	196	2	E75612	hypothetical prote	177	56	12.1	596	2	D70178	PTS system, fructo
105	58	12.6	215	2	A70650	probable membrane	178	56	12.1	596	2	C69451	cationic amino aci
106	58	12.6	257	2	A64459	diphthine synthase	179	56	12.1	1118	2	C95385	probable adenylate
107	58	12.6	277	2	S42452	raffinose operon r	180	56	12.1	1305	2	AB0168	probable cell divi
108	58	12.6	368	2	T26425	hypothetical prote	181	56	12.1	2055	2	T30259	multiple PDZ domai
109	58	12.6	376	2	AH1795	hypothetical membr	182	56	12.1	3339	2	T42205	breast cancer susc
110	58	12.6	398	2	A82081	cell division prot	183	56	12.1	5170	2	T15348	hypothetical prote
111	58	12.6	462	2	T75588	probable kynurenin	184	55.5	12.0	245	2	A90527	hypothetical prote
112	58	12.6	4836	2	T14346	herc2 protein - mo	185	55.5	12.0	249	4	T44821	bacteriorhodopsin
113	57.5	12.5	71	2	D23876	vitellogenin B2 pr	186	55.5	12.0	254	4	T75496	conserved hypothet
114	57.5	12.5	139	2	A70685	hypothetical prote	187	55.5	12.0	256	2	E75401	hypothetical prote
115	57.5	12.5	324	2	T36805	conserved hypothet	188	55.5	12.0	259	4	T44820	bacteriorhodopsin
116	57.5	12.5	342	2	A47673	photosystem II chl	189	55.5	12.0	262	1	RAH58	bacteriorhodopsin
117	57.5	12.5	356	2	T72475	hypothetical prote	190	55.5	12.0	262	2	H84300	bacteriorhodopsin
118	57.5	12.5	374	2	T10415	virus envelope pro	191	55.5	12.0	270	2	B29394	pancreatic elascas
119	57.5	12.5	461	2	B83601	probable transport	192	55.5	12.0	299	2	B83243	hypothetical prote
120	57.5	12.5	461	2	AF0579	C4-dicarboxylate a	193	55.5	12.0	309	2	C95138	tagatose-6-phospha
121	57.5	12.5	523	2	B83629	probable ATP-bindi	194	55.5	12.0	309	2	A98006	tagatose-6-phospha
122	57.5	12.5	528	2	T84205	potassium channel	195	55.5	12.0	316	2	G75388	hypothetical prote
123	57.5	12.5	594	2	B90586	transport protein	196	55.5	12.0	317	2	S16299	exoz protein - Rhi
124	57.5	12.5	636	2	S47299	gene F protein - r	197	55.5	12.0	317	2	B95975	acetyltransferase
125	57.5	12.5	662	2	T44219	hypothetical prote	198	55.5	12.0	344	2	S42648	photosystem II chl
126	57.5	12.5	662	2	T44034	hypothetical prote	199	55.5	12.0	344	2	AB2306	photosystem II chl
127	57.5	12.5	1902	1	B44858	lactocepin (EC 3.4	200	55.5	12.0	346	2	C71042	probable threonine
128	57	12.4	148	2	C84690	probable membrane	201	55.5	12.0	376	2	F72868	occlusion-derived
129	57	12.4	185	2	JN0786	adrenomedullin pre	202	55.5	12.0	383	2	S53379	probable membrane
130	57	12.4	258	2	F17251	probable uridine p	203	55.5	12.0	385	2	F86464	hypothetical prote
131	57	12.4	269	2	AG2268	hypothetical prote	204	55.5	12.0	389	2	B81347	probable aspartate
132	57	12.4	342	2	A30189	iron stress-induce	205	55.5	12.0	456	2	T22347	hypothetical prote
133	57	12.4	374	2	T05660	hypothetical prote	206	55.5	12.0	459	2	D86669	amino acid permeas
134	57	12.4	374	2	T00551	nodulin-like prote	207	55.5	12.0	545	2	AI2327	hypothetical prote
135	57	12.4	385	2	T04725	hypothetical prote	208	55.5	12.0	609	2	S28283	hypothetical prote
136	57	12.4	440	2	H86312	F2H15.2 protein -	209	55.5	12.0	625	2	SI3319	potassium channel
137	57	12.4	456	2	R96902	membrane protein,	210	55.5	12.0	648	2	C71658	probable primosoma
138	57	12.4	457	2	B64769	proline transport	211	55.5	12.0	716	2	T03695	delta 1 pyrroline-
139	57	12.4	457	2	D90685	proline permease t	212	55.5	12.0	851	2	T12503	hypothetical prote
140	57	12.4	457	2	H85535	proline permease t	213	55.5	12.0	946	1	A29550	methylenetetrahydr
141	57	12.4	461	2	D90711	C4-dicarboxylate a	214	55.5	12.0	1217	2	T22672	hypothetical prote
142	57	12.4	461	2	C64796	dcuC protein - Esc	215	55.5	12.0	1423	2	A49206	exo-beta-D-fructos
143	57	12.4	461	2	H85561	transport of dicar	216	55.5	12.0	2054	2	T46612	multi PDZ domain p
144	57	12.4	487	2	S73277	photosystem II 44K	217	55	11.9	52	2	T32956	hypothetical prote
145	56.5	12.3	114	2	E43559	homeotic protein R	218	55	11.9	52	2	T33694	hypothetical prote
146	56.5	12.3	187	2	S70186	21K protein - Shig	219	55	11.9	128	2	F71371	hypothetical prote
147	56.5	12.3	191	2	AD0905	probable exported	220	55	11.9	169	2	S18653	hypothetical prote
148	56.5	12.3	233	2	F70668	probable lipoprote	221	55	11.9	212	2	E82125	conserved hypothet
149	56.5	12.3	258	2	D84336	uridine phosphoryl	222	55	11.9	268	2	S05471	embryonic abundant
150	56.5	12.3	361	2	S19552	potassium channel	223	55	11.9	268	2	SI4068	seed protein precu
151	56.5	12.3	419	2	S22136	endothiapepsin (EC	224	55	11.9	288	2	T12462	hypothetical prote
152	56.5	12.3	471	2	T04911	hypothetical prote	225	55	11.9	312	2	B75405	endopeptidase-rela
153	56.5	12.3	485	2	E97506	potassium uptake p	226	55	11.9	334	2	S54438	hemin permease [va
154	56.5	12.3	500	2	F97025	spovB related memb	227	55	11.9	336	2	AH0201	probable Zinc-bind
155	56.5	12.3	614	2	A69845	Na+/H+ antiporter	228	55	11.9	340	2	AF2896	hypothetical prote
156	56.5	12.3	670	1	E70040	conserved hypothet	229	55	11.9	340	2	H97671	hypothetical prote
157	56.5	12.3	686	1	VGBENA	glycoprotein H pre	230	55	11.9	344	2	E84043	glyceraldehyde-3-p
158	56.5	12.3	686	1	VGBEPK	glycoprotein H pre	231	55	11.9	357	2	A23641	RP2 protein, testo
159	56.5	12.3	686	2	S15478	glycoprotein H - s	232	55	11.9	376	1	S17246	chorismate synthas
160	56.5	12.3	852	2	S25359	hypothetical prote	233	55	11.9	404	2	S34031	KTR3 protein - yea
161	56	12.1	79	1	TIEPVK	K+ channel blocker	234	55	11.9	410	2	AH2895	hypothetical prote
162	56	12.1	196	2	F64231	hypothetical prote	235	55	11.9	410	2	C97671	probable maltose-b
163	56	12.1	222	2	F82353	conserved hypothet	236	55	11.9	443	2	B86180	protein TlG11.3 [i
164	56	12.1	261	2	B82966	conserved hypothet	237	55	11.9	459	2	AH7201	conserved hypothet
165	56	12.1	281	2	B98317	ATP synthase chain	238	55	11.9	461	2	S57713	probable mannosyl
166	56	12.1	388	2	T09885	hypothetical prote	239	55	11.9	473	1	F2KK4C	photosystem II chl
167	56	12.1	411	2	C87586	metal ion efflux m	240	55	11.9	482	2	AG1147	P60 extracellular
168	56	12.1	436	2	G70058	hypothetical prote	241	55	11.9	484	2	A41487	protein P60 precur
169	56	12.1	440	2	C97376	probable transport	242	55	11.9	654	2	A96235	hydroxamate-depend
170	56	12.1	440	2	AI2593	MFS permease limpo	243	55	11.9	654	2	AC3051	hypothetical prote
171	56	12.1	449	2	H70546	hypothetical prote	244	55	11.9	716	2	E96772	penicillin-binding
172	56	12.1	503	2	S36514	Li protein - human	245	55	11.9	2331	2	S18188	notch protein homo
173	56	12.1	547	2	D95337	probable manganese	246	55	11.9	2531	2	A46019	notch-1 protein -
174	56	12.1	558	2	S29125	dimethylaniline mo	247	54.5	11.8	173	2	S33295	translocon-associa
175	56	12.1	578	2	B37852	phosphotransferase	248	54.5	11.8	177	2	G75285	hypothetical prote



249 54.5 11.8 185 2 T51844 RING-H2 finger pro  
 250 54.5 11.8 204 2 AC1961 ATP-dependent Clp  
 251 54.5 11.8 226 2 S76020 endopeptidase Clp  
 252 54.5 11.8 255 2 P86203 hypothetical prote  
 253 54.5 11.8 269 2 T19947 hypothetical prote  
 254 54.5 11.8 276 2 AC1838 hypothetical prote  
 255 54.5 11.8 282 2 P00376 cell fusion glycop  
 256 54.5 11.8 296 2 P81145 probable epoxide h  
 257 54.5 11.8 296 2 A85698 transposase for IS  
 258 54.5 11.8 296 2 A99840 transposase for IS  
 259 54.5 11.8 304 2 S59965 phosphotransferase  
 260 54.5 11.8 337 2 G87487 conserved hypothet  
 261 54.5 11.8 362 2 S77244 biotin synthase (E  
 262 54.5 11.8 369 2 E81722 hypothetical prote  
 263 54.5 11.8 373 2 G85355 nodulin-like prote  
 264 54.5 11.8 393 2 A80035 cystathionine beta  
 265 54.5 11.8 422 2 T07967 mandelonitrile ly  
 266 54.5 11.8 445 1 S54140 D-serine permease  
 267 54.5 11.8 458 1 YTSRRT tetracycline resis  
 268 54.5 11.8 458 1 YTSOG tetracycline resis  
 269 54.5 11.8 458 2 JQ1211 tetracycline resis  
 270 54.5 11.8 458 2 S23743 tetracycline resis  
 271 54.5 11.8 483 1 A53595 allantoinase (EC 3  
 272 54.5 11.8 484 2 T00158 amidase (EC 3.5.-.  
 273 54.5 11.8 501 2 E87239 aldehyde dehydroge  
 274 54.5 11.8 576 2 A49933 proteinase SM tran  
 275 54.5 11.8 586 2 T48672 ABC-type transport  
 276 54.5 11.8 622 2 AC1236 acyltransferase (t  
 277 54.5 11.8 628 2 T01467 hypothetical prote  
 278 54.5 11.8 722 2 E91339 probable peptidase  
 279 54.5 11.8 735 2 E69133 hypothetical prote  
 280 54.5 11.8 895 2 S43433 dyscroglycan - hum  
 281 54.5 11.8 895 2 S20582 dytrophin-associat  
 282 54.5 11.8 900 2 G87431 pyruvate phosphate  
 283 54.5 11.8 1044 2 T31072 heterocyst differe  
 284 54.5 11.8 1099 2 T14850 S-layer protein pr  
 285 54.5 11.8 1146 2 B35962 protein-tyrosine k  
 286 54.5 11.8 1182 2 A35962 protein-tyrosine k  
 287 54.5 11.8 98 2 T17183 NADH2 dehydrogenas  
 288 54.5 11.7 98 2 T17348 NADH2 dehydrogenas  
 289 54 11.7 154 1 MWBEI6 16.9K membrane pro  
 290 54 11.7 168 2 S47881 NADH2 dehydrogenas  
 291 54 11.7 188 2 A75382 NADH2 dehydrogenas  
 292 54 11.7 248 1 PRMSC2 granzyme C (EC 3.4  
 293 54 11.7 259 2 C64481 conserved hypothet  
 294 54 11.7 292 2 T14627 hypothetical prote  
 295 54 11.7 316 2 F91044 transaldolase A [i  
 296 54 11.7 316 2 A85889 transaldolase A [i  
 297 54 11.7 316 2 G65021 transaldolase (EC  
 298 54 11.7 316 2 G65021 hypothetical prote  
 299 54 11.7 328 2 A69218 cysteine proteinas  
 300 54 11.7 346 2 C86413 rod outer segment  
 301 54 11.7 351 2 I68620 cysteine proteinas  
 302 54 11.7 356 2 S66348 hypothetical prote  
 303 54 11.7 356 2 B97742 hypothetical prote  
 304 54 11.7 359 2 F69061 hypothetical prote  
 305 54 11.7 386 2 A72313 cell division prot  
 306 54 11.7 394 2 C64185 gene IV protein -  
 307 54 11.7 428 2 S08084 UDP-N-acetylglucos  
 308 54 11.7 440 2 E84118 proline-specific P  
 309 54 11.7 456 2 AH0551 hypothetical prote  
 310 54 11.7 476 2 T40086 peptidase-binding pr  
 311 54 11.7 549 2 C86692 glycerol 3 phospho  
 312 54 11.7 558 1 AE1236 INDA1 protein - fu  
 313 54 11.7 573 2 S33212 hypothetical prote  
 314 54 11.7 604 2 B84221 hypothetical prote  
 315 54 11.7 625 2 T25373 hypothetical prote  
 316 54 11.7 634 2 T33528 probable glycosyl  
 317 54 11.7 787 2 T38224 probable protein k  
 318 54 11.7 869 2 A96558 regulatory protein  
 319 54 11.7 880 2 S49627 aminopeptidase N p  
 320 54 11.7 885 2 G83260

322 54 11.7 909 2 T00009 probable primase (  
 323 54 11.7 967 2 T40889 sarcosine oxidase  
 324 54 11.7 993 2 A38437 probable homeotic  
 325 54 11.7 1072 2 T50949 verprolin related  
 326 54 11.7 1222 2 G72614 probable reverse g  
 327 54 11.7 1283 2 T18939 hypothetical prote  
 328 53.5 11.6 114 2 C90344 oleosin-like prote  
 329 53.5 11.6 153 2 T49895 hypothetical prote  
 330 53.5 11.6 173 2 S01145 CDP-diacylglycerol  
 331 53.5 11.6 211 2 G82573 epsilonon-crystallin  
 332 53.5 11.6 225 1 CYPGE uncharacterized me  
 333 53.5 11.6 269 2 D96957 cell fusion glycop  
 334 53.5 11.6 282 2 P00388 IS629 transposase  
 335 53.5 11.6 296 2 C90978 IS629 transposase  
 336 53.5 11.6 296 2 H85824 trypsin homolog -  
 337 53.5 11.6 303 2 T13598 conserved hypothet  
 338 53.5 11.6 307 2 B87232 hypothetical prote  
 339 53.5 11.6 339 2 H71285 probable cydB prot  
 340 53.5 11.6 346 2 D70558 chorismate synthas  
 341 53.5 11.6 357 2 F81679 multidrug-efflux t  
 342 53.5 11.6 376 2 AP1943 hypothetical prote  
 343 53.5 11.6 378 2 T34372 hypothetical prote  
 344 53.5 11.6 383 2 T48018 transcription fact  
 345 53.5 11.6 410 2 A48585 macrolide-efflux p  
 346 53.5 11.6 412 2 AH3274 photosystem II chl  
 347 53.5 11.6 461 2 T06936 potassium channel  
 348 53.5 11.6 495 2 I57680 potassium channel  
 349 53.5 11.6 495 2 A40090 potassium channel  
 350 53.5 11.6 495 2 B39113 hypothetical prote  
 351 53.5 11.6 529 2 H84049 hypothetical prote  
 352 53.5 11.6 539 2 T32693 gene F protein - r  
 353 53.5 11.6 546 2 S47300 cell fusion glycop  
 354 53.5 11.6 553 1 VGN2MV tegument protein -  
 355 53.5 11.6 556 2 T03114 probable transport  
 356 53.5 11.6 571 1 H65169 probable cotranspo  
 357 53.5 11.6 571 2 F86052 probable cotranspo  
 358 53.5 11.6 594 2 T43246 amino acid transpo  
 359 53.5 11.6 597 2 AH2351 serine/threonine k  
 360 53.5 11.6 890 2 T35237 probable secreted  
 361 53.5 11.6 945 2 S30398 aminopeptidase N h  
 362 53.5 11.6 985 2 T10339 DNA-directed DNA p  
 363 53.5 11.6 1045 2 E90705 hypothetical prote  
 364 53.5 11.6 1045 2 H85555 hypothetical prote  
 365 53.5 11.6 1047 2 E64790 ybde protein - Esc  
 366 53.5 11.6 1075 2 S76433 cation efflux syst  
 367 53.5 11.6 1175 2 S51005 protein-tyrosine-p  
 368 53.5 11.6 2037 2 T16881 hypothetical prote  
 369 53.5 11.6 3566 1 A40701 tenascin-X precurs  
 370 53.5 11.6 90 2 T33692 hypothetical prote  
 371 53 11.5 148 2 A84636 similar to avrRpt2  
 372 53 11.5 154 1 F70002 NADH2 dehydrogenas  
 373 53 11.5 166 2 D58889 conserved hypothet  
 374 53 11.5 201 2 A71124 hypothetical prote  
 375 53 11.5 202 2 JC6205 cell surface anti g  
 376 53 11.5 214 2 JC5448 serine proteinase  
 377 53 11.5 216 2 AH0265 probable membrane  
 378 53 11.5 216 2 JC7930 small neutral amin  
 379 53 11.5 224 2 S7949 beta-tubulin ASL1  
 380 53 11.5 224 2 S73823 MG243 homolog H91  
 381 53 11.5 257 2 D71544 hypothetical prote  
 382 53 11.5 264 2 A75076 membrane protein P  
 383 53 11.5 279 2 A95933 probable inositol  
 384 53 11.5 300 2 B83100 inhibitor of chrom  
 385 53 11.5 306 2 A88040 protein F47F6.1 [i  
 386 53 11.5 310 2 D87704 integral membrane  
 387 53 11.5 339 2 AG0165 L-allo-threonine a  
 388 53 11.5 342 2 A4965 cysteine proteinas  
 389 53 11.5 342 2 A45524 anthranilate phosph  
 390 53 11.5 364 2 AH1857 probable sugar ABC  
 391 53 11.5 376 2 E58879 geranylgeranyl-dip  
 392 53 11.5 377 2 A53044 probable membrane  
 393 53 11.5 385 2 A91178

395	53	11.5	385	2	B86024	probable membrane	468	52.5	11.4	409	2	T47644	protein phosphatase
396	53	11.5	385	2	S47733	YhiU protein precursor	469	52.5	11.4	410	2	B48585	transcription factor
397	53	11.5	386	2	A26017	patatin F5 precursor	470	52.5	11.4	421	2	T35515	hypothetical protein
398	53	11.5	403	2	B69873	cell-division protein	471	52.5	11.4	422	2	JE0239	lin-10 protein - r
399	53	11.5	405	2	S61551	breast-regressing	472	52.5	11.4	422	2	B82904	hypothetical protein
400	53	11.5	409	2	F83493	probable MFS trans	473	52.5	11.4	429	2	AF0681	probable voltage g
401	53	11.5	418	2	H82087	NupC family protein	474	52.5	11.4	429	2	S30049	transcription factor
402	53	11.5	426	2	B82712	ATP-dependent Clp	475	52.5	11.4	452	2	G95356	probable oxidoredu
403	53	11.5	438	2	G87675	arylesterase-relat	476	52.5	11.4	500	2	H70629	probable AMINOPEPT
404	53	11.5	447	2	H86534	hypothetical protein	477	52.5	11.4	514	2	T21286	hypothetical protein
405	53	11.5	447	2	H72089	hypothetical protein	478	52.5	11.4	523	2	SS3401	probable membrane
406	53	11.5	463	2	B81580	hypothetical protein	479	52.5	11.4	533	1	YRMSCS	monophenol monooxy
407	53	11.5	469	1	AJEBOT	glutamate-ammonia	480	52.5	11.4	542	2	AH2191	hypothetical protein
408	53	11.5	469	2	A10949	glutamine syntheta	481	52.5	11.4	542	2	A13564	hypothetical membr
409	53	11.5	469	2	S23899	glutamate-ammonia	482	52.5	11.4	545	2	B32688	beta-galactosidase
410	53	11.5	471	2	S78347	photosystem II chl	483	52.5	11.4	549	2	G91178	cycloplasmic trehal
411	53	11.5	515	2	B84406	TRK potassium upta	484	52.5	11.4	549	2	H86024	cytoplasmic trehal
412	53	11.5	581	2	T38501	hypothetical protein	485	52.5	11.4	549	2	S47739	probable alpha,alp
413	53	11.5	586	2	T20036	hypothetical protein	486	52.5	11.4	572	2	A55676	excitatory amino a
414	53	11.5	588	2	AC2276	oligopeptide bindi	487	52.5	11.4	652	2	AH2245	thiamin biosynthes
415	53	11.5	605	2	E89153	cadmium efflux ATP	488	52.5	11.4	657	1	A64079	2',3'-cyclic-nucle
416	53	11.5	610	2	A55939	dihydrolipoamide S	489	52.5	11.4	686	2	T06700	hypothetical protein
417	53	11.5	618	2	A13303	hypothetical protein	490	52.5	11.4	699	2	T12170	NADH2 dehydrogenas
418	53	11.5	637	2	T49099	dihydrolipoamide S	491	52.5	11.4	699	2	T12172	NADH2 dehydrogenas
419	53	11.5	653	2	A83154	probable choline t	492	52.5	11.4	795	1	SVECFB	phenylalanine-tRNA
420	53	11.5	656	2	T52064	dnaJ-like protein	493	52.5	11.4	795	1	H85779	phenylalanine-tRNA
421	53	11.5	728	2	D86278	hypothetical protein	494	52.5	11.4	795	1	SVECFB	phenylalanine-tRNA
422	53	11.5	770	2	T23999	hypothetical protein	495	52.5	11.4	795	1	D90931	phenylalanine-tRNA
423	53	11.5	776	2	T02584	probable protein k	496	52.5	11.4	803	2	F83360	Glucose dehydrogen
424	53	11.5	1005	2	B82969	sarcosine oxidase	497	52.5	11.4	826	2	E90289	malate synthase, p
425	53	11.5	1070	2	J04593	protein-tyrosine k	498	52.5	11.4	883	2	AE0207	conserved hypothet
426	53	11.5	1162	2	E84431	probable Na+/H+ an	499	52.5	11.4	977	2	T41289	hypothetical protein
427	53	11.5	1176	2	I58345	protein tyrosine p	500	52.5	11.4	1011	2	T40851	hypothetical protein
428	53	11.5	1240	1	DJBE21	DNA-directed DNA p	501	52.5	11.4	1205	1	T18517	hypothetical protein
429	53	11.5	1250	2	T00454	hypothetical protein	502	52.5	11.4	1225	1	S24284	DNA-directed DNA p
430	53	11.5	1305	2	T23314	hypothetical protein	503	52.5	11.4	1225	2	A36607	hypothetical protein
431	53	11.5	1326	2	B56395	secretory phosphol	504	52.5	11.4	1345	1	VCBEH6	hypothetical protein
432	53	11.5	1331	2	S05011	calcium channel al	505	52.5	11.4	1453	2	S41453	conserved hypothet
433	53	11.5	1465	2	A56395	secretory phosphol	506	52.5	11.4	1541	2	T30227	regulatory protein
434	53	11.5	1529	2	T16779	hypothetical protein	507	52.5	11.4	1544	2	T29482	regulatory protein
435	53	11.5	2143	2	JH0427	voltage-dependent	508	52.5	11.4	2285	1	G02434	hypothetical protein
436	53	11.5	2166	2	S11339	calcium channel pr	509	52	11.3	119	2	D64611	hypothetical protein
437	53	11.5	2171	2	S05054	calcium channel al	510	52	11.3	122	2	F75351	hypothetical protein
438	53	11.5	2599	2	A96616	unknown protein F1	511	52	11.3	148	2	D64356	conserved hypothet
439	52.5	11.4	71	2	I50439	vitellogenin III -	512	52	11.3	160	2	G95113	regulatory protein
440	52.5	11.4	78	2	G84333	hypothetical protein	513	52	11.3	160	2	H97982	regulatory protein
441	52.5	11.4	159	2	E85360	ribosomal protein	514	52	11.3	175	2	AE1508	hypothetical protein
442	52.5	11.4	165	2	C72116	hypothetical protein	515	52	11.3	202	2	JC4635	tumor-associated L
443	52.5	11.4	210	2	A83516	probable outer mem	516	52	11.3	207	2	T45600	hypothetical protein
444	52.5	11.4	219	2	F75402	probable competenc	517	52	11.3	219	2	G97271	probable phosphogl
445	52.5	11.4	219	2	AC1881	hypothetical protein	518	52	11.3	235	2	B82173	pseudouridine synt
446	52.5	11.4	244	2	S29982	class II histocomp	519	52	11.3	238	2	C82866	conjugal transfer
447	52.5	11.4	245	2	S29980	class II histocomp	520	52	11.3	260	2	I56559	neurospain - mouse
448	52.5	11.4	256	2	S14518	chlorophyll a/b-bi	521	52	11.3	262	2	B81200	conserved hypothet
449	52.5	11.4	257	2	S29981	class II histocomp	522	52	11.3	265	2	D83761	hypothetical protein
450	52.5	11.4	285	1	A43556	homeotic protein H	523	52	11.3	291	2	B75618	chromosome partiti
451	52.5	11.4	289	1	A43556	dihydrodipicolinat	524	52	11.3	295	2	B85661	probable transposa
452	52.5	11.4	296	2	S09261	probable transposa	525	52	11.3	297	2	T47857	myb protein-like -
453	52.5	11.4	301	2	B84189	glycine cleavage s	526	52	11.3	310	2	S46239	ribosome-inactivat
454	52.5	11.4	309	2	A87564	membrane protein,	527	52	11.3	320	2	T32006	hypothetical protein
455	52.5	11.4	310	2	C39778	tagatose-6-phospha	528	52	11.3	320	2	A12305	hypothetical protein
456	52.5	11.4	310	2	T31125	hypothetical protein	529	52	11.3	327	2	AH2608	transcription regu
457	52.5	11.4	322	2	AF1031	conserved hypothet	530	52	11.3	327	2	G97390	araC family transac
458	52.5	11.4	332	2	C72310	hypothetical protein	531	52	11.3	359	2	A43532	hypothetical protein
459	52.5	11.4	334	2	D81217	hypothetical protein	532	52	11.3	364	2	B71139	probable membrane
460	52.5	11.4	334	2	T33950	hypothetical protein	533	52	11.3	372	2	B64819	hypothetical protein
461	52.5	11.4	342	2	C48435	cysteine proteinas	534	52	11.3	372	2	B85591	hypothetical protein
462	52.5	11.4	356	2	D84280	hypothetical protein	535	52	11.3	372	2	G90740	hypothetical 41.1K
463	52.5	11.4	360	2	T51344	RNA helicase RH18	536	52	11.3	375	2	S47704	probable transport
464	52.5	11.4	366	2	A49877	prostaglandin F re	537	52	11.3	375	2	F91173	probable transport
465	52.5	11.4	377	2	C69758	amino acid transpo	538	52	11.3	375	2	F86019	probable transport
466	52.5	11.4	394	2	B86507	hypothetical protein	539	52	11.3	397	2	F83152	hypothetical protein
467	52.5	11.4	394	2	B81554	hypothetical protein	540	52	11.3	397	2	B70048	conserved hypothet

541	52	11.3	417	2	E69804	multidrug resistan	614	51.5	11.2	410	2	S45894	regulatory protein
542	52	11.3	457	2	S39079	puff C-8 protein -	615	51.5	11.2	429	2	P87038	probable membrane
543	52	11.3	469	2	D81017	chloride channel p	616	51.5	11.2	438	2	A83037	probable MFS trans
544	52	11.3	470	2	T070641	hypothetical prote	617	51.5	11.2	450	2	C36704	unknown protein, 2
545	52	11.3	491	2	S75449	hypothetical prote	618	51.5	11.2	451	2	P75177	tryptophan synthas
546	52	11.3	502	2	G87433	conserved hypotet	619	51.5	11.2	474	1	A40570	lipoprotein lipase
547	52	11.3	502	2	T29729	hypothetical prote	620	-51.5	11.2	478	1	C42790	cystathionine beta
548	52	11.3	526	2	H85891	hydrogenase 4 memb	621	51.5	11.2	478	2	T30763	hypothetical prote
549	52	11.3	526	2	D91047	hydrogenase 4 memb	622	51.5	11.2	478	2	T32476	probable protein-t
550	52	11.3	530	2	D87255	apolipoprotein N-a	623	51.5	11.2	481	2	B82130	pyruvate kinase II
551	52	11.3	534	2	T27054	hypothetical prote	624	51.5	11.2	493	2	T21445	hypothetical prote
552	52	11.3	544	2	T17422	halogenase-like pr	625	51.5	11.2	509	2	G82409	glyceraldenhyde 3-p
553	52	11.3	548	2	C83698	electron transfer	626	51.5	11.2	513	2	T34546	hypothetical prote
554	52	11.3	553	2	S75892	probable glycerol-	627	51.5	11.2	525	2	A70735	probable guaA prot
555	52	11.3	567	2	H87370	major facilitator	628	51.5	11.2	531	2	D96965	PTS system, arbuti
556	52	11.3	573	2	A33533	cell surface glyco	629	51.5	11.2	534	1	JU0274	cell fusion glycop
557	52	11.3	579	2	A64100	inner membrane cop	630	51.5	11.2	536	2	D81700	CTP synthase TC045
558	52	11.3	635	2	H69626	PTS fructose-speci	631	51.5	11.2	536	2	P85697	hypothetical prote
559	52	11.3	706	2	H81943	probable polyribon	632	51.5	11.2	536	2	D64865	probable Na+/H+-ex
560	52	11.3	707	2	C81161	polynucleotide	633	51.5	11.2	536	2	P90839	hypothetical prote
561	52	11.3	733	2	F82965	hypothetical prote	634	51.5	11.2	540	1	JU0470	site-specific DNA-
562	52	11.3	738	2	S37876	glutamine-rich pro	635	51.5	11.2	541	1	A70022	multidrug-efflux t
563	52	11.3	773	2	AH2061	hypothetical prote	636	51.5	11.2	541	2	JN0511	heat shock protein
564	52	11.3	823	2	A96737	hypothetical prote	637	51.5	11.2	547	2	T46059	MAP kinase [import
565	52	11.3	840	2	T21333	hypothetical prote	638	51.5	11.2	549	2	T51099	cell fusion glycop
566	52	11.3	869	2	A95156	conserved hypotet	639	51.5	11.2	550	1	E48556	conserved hypotet
567	52	11.3	878	2	D98022	conserved hypotet	640	51.5	11.2	558	2	C72391	interferon alpha r
568	52	11.3	906	2	A82533	hypothetical prote	641	51.5	11.2	560	2	S27387	cystathionine beta
569	52	11.3	1016	2	T00375	hypothetical prote	642	51.5	11.2	561	1	A42790	probable membrane
570	52	11.3	1017	2	T37201	hypothetical prote	643	51.5	11.2	623	2	T35377	transketolase (EC
571	52	11.3	1106	2	A97647	cation efflux syst	644	51.5	11.2	666	2	P0815	transketolase 2 is
572	52	11.3	1106	2	AG2870	Acr family transpo	645	51.5	11.2	667	1	A48660	transketolase 2 is
573	52	11.3	1146	2	T05112	probable sensor ki	646	51.5	11.2	667	2	G91044	transketolase 2 is
574	52	11.3	1146	2	A82174	sensory box sensor	647	51.5	11.2	667	2	B85889	transketolase 2 is
575	52	11.3	1484	2	C97196	probable membrane	648	51.5	11.2	672	2	T12715	transketolase 2 is
576	52	11.3	1957	2	S68453	sodium channel pro	649	51.5	11.2	724	2	T19601	transketolase 2 is
577	52	11.3	2139	2	A44467	voltage-dependent	650	51.5	11.2	726	2	T31287	transketolase 2 is
578	52	11.3	2220	2	A45290	calcium channel pr	651	51.5	11.2	763	2	A13443	transketolase 2 is
579	52	11.3	3429	2	T13853	hypothetical prote	652	51.5	11.2	765	2	B75288	transketolase 2 is
580	51.5	11.2	116	2	A83693	transcription regu	653	51.5	11.2	795	2	A50705	phenylalanyl-tRNA
581	51.5	11.2	121	1	PSABA	phospholipase A2 (	654	51.5	11.2	829	2	T29372	hypothetical prote
582	51.5	11.2	132	2	C72563	hypothetical prote	655	51.5	11.2	846	2	T27282	hypothetical prote
583	51.5	11.2	146	2	S42570	flavodoxin - Desul	656	51.5	11.2	869	2	C56617	ciaC protein precu
584	51.5	11.2	167	2	H87874	VP829-like phospho	657	51.5	11.2	1451	1	JQ1719	E2 glycoprotein pr
585	51.5	11.2	172	2	F75491	conserved hypotet	658	51.5	11.2	1755	2	T51532	hypothetical prote
586	51.5	11.2	209	1	A40173	orotate phosphorib	659	51.5	11.2	1784	2	T43167	sodium channel pro
587	51.5	11.2	206	2	T00733	hypothetical prote	660	51.5	11.2	2301	1	GNNYTM	genome polyprotein
588	51.5	11.2	212	2	H64495	dual specificity p	661	51.5	11.2	2303	1	GNNYTM	genome polyprotein
589	51.5	11.2	222	2	H64495	cobalamin biosynth	662	51.5	11.2	89	2	AH3403	hypothetical prote
590	51.5	11.2	270	2	A29934	pancreatic elastas	663	51.5	11.1	93	2	A86491	conserved hypotet
591	51.5	11.2	276	2	A70425	hypothetical prote	664	51.5	11.1	93	2	P72130	hypothetical prote
592	51.5	11.2	282	2	AC2294	hypothetical prote	665	51.5	11.1	95	2	AG2439	hypothetical prote
593	51.5	11.2	289	2	G97192	oligopeptide ABC-t	666	51.5	11.1	97	2	C75415	hypothetical prote
594	51.5	11.2	299	2	B95939	probable spermidin	667	51.5	11.1	106	2	A72588	hypothetical prote
595	51.5	11.2	299	2	H97884	hypothetical prote	668	51.5	11.1	152	2	H95153	conserved hypotet
596	51.5	11.2	312	2	B69170	UDP-N-acetylmuram	669	51.5	11.1	173	2	AF2518	conserved hypotet
597	51.5	11.2	313	2	S75329	hypothetical prote	670	51.5	11.1	188	2	T15651	hypothetical prote
598	51.5	11.2	314	2	T21971	hypothetical prote	671	51.5	11.1	201	2	E75039	multiple antibioti
599	51.5	11.2	319	2	T02691	glossyl protein gl	672	51.5	11.1	202	2	A81441	probable orotate p
600	51.5	11.2	342	2	T16806	hypothetical prote	673	51.5	11.1	204	2	A82389	cysteine proteinas
601	51.5	11.2	345	2	S76667	hypothetical prote	674	51.5	11.1	212	2	I67437	hypothetical prote
602	51.5	11.2	364	2	G82734	acetylmurithine de	675	51.5	11.1	221	2	S75146	hypothetical prote
603	51.5	11.2	366	2	I53488	prostaglandin F2 a	676	51.5	11.1	229	2	E85806	hypothetical prote
604	51.5	11.2	366	2	S51281	F2-alpha receptor	677	51.5	11.1	240	2	T02059	hypothetical prote
605	51.5	11.2	370	2	AH1485	fructose-specific	678	51.5	11.1	246	2	S26826	hypothetical prote
606	51.5	11.2	370	2	AH1124	fructose-specific	679	51.5	11.1	246	2	T28166	hypothetical prote
607	51.5	11.2	376	2	A75381	peptide ABC transp	680	51.5	11.1	261	2	A71192	GTP-binding regula
608	51.5	11.2	380	2	D83174	probable acetylpol	681	51.5	11.1	263	2	AG2280	histone H1, maize
609	51.5	11.2	381	2	A35300	G protein-coupled	682	51.5	11.1	264	2	G96978	hypothetical prote
610	51.5	11.2	381	2	F87553	aminotransferase,	683	51.5	11.1	265	2	B81229	hypothetical prote
611	51.5	11.2	382	2	G84971	Edg-like porin (i	684	51.5	11.1	265	2	A82000	hypothetical prote
612	51.5	11.2	383	2	I53870	Edg-1 orphan recep	685	51.5	11.1	265	2	S03328	GTP-binding regula
613	51.5	11.2	390	2	C95954	hypothetical prote	686	51.5	11.1	268	2		histone H1, maize

687	51	11.1	279	2	T22051	hypothetical prote	760	50.5	11.0	173	2	SS9864	TRAP-like protein
688	51	11.1	282	2	E64063	hypothetical prote	761	50.5	11.0	201	1	IMBPSB	immunity protein -
689	51	11.1	282	2	A41023	aspergillopepsin I	762	50.5	11.0	204	2	E83036	hypothetical prote
690	51	11.1	285	2	T15498	hypothetical prote	763	50.5	11.0	208	2	F71314	probable transcrip
691	51	11.1	295	2	F90938	hypothetical prote	764	50.5	11.0	217	2	I51062	MHC class II beta
692	51	11.1	295	2	B85664	transposase for IS	765	50.5	11.0	224	2	T34686	probable integral
693	51	11.1	295	2	D90801	hypothetical prote	766	50.5	11.0	227	2	T12797	immunity protein d
694	51	11.1	295	2	B85613	probable transposa	767	50.5	11.0	228	2	C28551	hypothetical prote
695	51	11.1	309	2	A80746	motility protein B	768	50.5	11.0	231	2	H81698	hypothetical prote
696	51	11.1	321	2	A50590	cathepsin O (EC 3.	769	50.5	11.0	233	2	JH0372	42K surface glycop
697	51	11.1	328	1	S64306	hypothetical prote	770	50.5	11.0	234	2	E95360	hypothetical prote
698	51	11.1	348	2	A06645	sermidine/putresc	771	50.5	11.0	240	1	T0EC34	transposase - Esch
699	51	11.1	355	2	E96785	protein F10A5.28 [	772	50.5	11.0	247	2	I51060	MHC class II beta
700	51	11.1	357	2	A71523	probable chorismat	773	50.5	11.0	247	2	I51059	MHC class II beta
701	51	11.1	361	2	A45211	prostaglandin E re	774	50.5	11.0	249	2	S75671	hypothetical prote
702	51	11.1	362	2	A33058	prostaglandin F2-a	775	50.5	11.0	249	2	H95256	ABC transporter, p
703	51	11.1	364	2	S65009	prostaglandin E re	776	50.5	11.0	250	2	T09160	proteasome subunit
704	51	11.1	365	2	A42414	prostaglandin E re	777	50.5	11.0	252	2	F70711	probable membranep
705	51	11.1	372	2	S75587	H+/Ca2+ exchanging	778	50.5	11.0	253	2	A98122	hypothetical prote
706	51	11.1	375	2	T03256	GTP-binding protei	779	50.5	11.0	255	2	JN0829	3alpha-hydroxyster
707	51	11.1	377	2	T04086	GTP-binding protei	780	50.5	11.0	258	2	A69805	hypothetical prote
708	51	11.1	377	2	T16985	GTP-binding protei	781	50.5	11.0	260	2	F82954	probable short-cha
709	51	11.1	379	2	A82423	hypothetical prote	782	50.5	11.0	264	2	D87504	hypothetical prote
710	51	11.1	384	2	A69622	ferrichrome ABC tr	783	50.5	11.0	286	2	E86844	shikimate 5-dehydr
711	51	11.1	394	2	B85535	probable transport	784	50.5	11.0	288	2	F85818	hypothetical prote
712	51	11.1	394	2	F90684	probable transport	785	50.5	11.0	293	2	A83623	hypothetical prote
713	51	11.1	402	2	B24941	NupC family protei	786	50.5	11.0	296	2	A85841	probable transposa
714	51	11.1	404	2	T39270	conserved hypothet	787	50.5	11.0	296	2	D91284	hypothetical prote
715	51	11.1	409	2	G90491	conserved hypothet	788	50.5	11.0	296	2	F90868	hypothetical prote
716	51	11.1	416	2	T14554	calreticulin - bee	789	50.5	11.0	296	2	D90995	hypothetical prote
717	51	11.1	418	2	S31124	hypothetical prote	790	50.5	11.0	296	2	E91020	hypothetical prote
718	51	11.1	421	2	B32062	conserved hypothet	791	50.5	11.0	296	2	A91132	hypothetical prote
719	51	11.1	423	2	A80054	probable Na+ depen	792	50.5	11.0	296	2	F91111	hypothetical prote
720	51	11.1	435	2	E71350	probable aspartate	793	50.5	11.0	296	2	G90998	hypothetical prote
721	51	11.1	439	2	S58327	cobalt accumulatio	794	50.5	11.0	296	2	T00240	transposase - Esch
722	51	11.1	439	2	T18898	hypothetical prote	795	50.5	11.0	296	2	B90837	hypothetical prote
723	51	11.1	440	2	AD1073	thymidine phosphor	796	50.5	11.0	296	2	C91065	hypothetical prote
724	51	11.1	449	2	C86496	hypothetical prote	797	50.5	11.0	296	2	H90779	hypothetical prote
725	51	11.1	449	2	D72127	hypothetical prote	798	50.5	11.0	296	2	C90906	hypothetical prote
726	51	11.1	449	2	A81544	hypothetical prote	799	50.5	11.0	296	2	A99972	hypothetical prote
727	51	11.1	450	2	AB1420	PTS cellobiose-spe	800	50.5	11.0	297	2	T09542	endonuclease G (EC
728	51	11.1	450	2	AC1795	tetracycline resist	801	50.5	11.0	297	2	T45436	hypothetical membr
729	51	11.1	458	1	Y7BSY8	photosystem II chl	802	50.5	11.0	302	2	S02728	hypothetical membr
730	51	11.1	460	2	S06469	aminopeptidase BH3	803	50.5	11.0	302	2	S60955	actinidin (EC 3.4
731	51	11.1	466	2	E84132	ammonium transport	804	50.5	11.0	313	2	AH1300	probable membrane
732	51	11.1	468	2	A84668	arginine/ornithine	805	50.5	11.0	314	2	F86928	malonyl CoA-acyl c
733	51	11.1	485	2	A72006	Ammonium transport	806	50.5	11.0	317	2	T27994	34 kDa antigen (im
734	51	11.1	514	2	A96671	cytochrome-c oxida	807	50.5	11.0	324	2	A86639	hypothetical prote
735	51	11.1	516	2	T09859	cytochrome-c oxida	808	50.5	11.0	327	2	S61982	conserved hypothet
736	51	11.1	525	2	T00459	hypothetical prote	809	50.5	11.0	332	2	S77386	nitrate transport
737	51	11.1	528	2	T22583	hypothetical prote	810	50.5	11.0	332	2	C71390	NADH2 dehydrogenas
738	51	11.1	531	2	T12406	cytochrome-c oxida	811	50.5	11.0	346	2	A69808	H+/Ca2+ exchanger
739	51	11.1	560	2	T51485	sugar transporter-	812	50.5	11.0	351	1	BVECMG	UDP-N-acetylglucos
740	51	11.1	616	2	T07611	aconitate hydratase	813	50.5	11.0	355	2	F85491	hypothetical prote
741	51	11.1	635	1	A64162	cytochrome c-type	814	50.5	11.0	355	2	F90640	hypothetical prote
742	51	11.1	639	2	J00607	glucan 1,4-alpha-g	815	50.5	11.0	361	2	F87286	cation efflux fami
743	51	11.1	699	2	A96802	unknown protein (i	816	50.5	11.0	362	2	JC7559	sphingosine 1-phos
744	51	11.1	745	1	A70458	phosphoribosylform	817	50.5	11.0	364	2	H70776	hypothetical prote
745	51	11.1	749	1	A93329	phosphoribosylform	818	50.5	11.0	377	2	B53044	geranylgeranyl-dip
746	51	11.1	754	2	S37403	transcription fact	819	50.5	11.0	379	2	T45768	protein phosphatas
747	51	11.1	770	2	T50308	probable translati	820	50.5	11.0	382	2	H90500	Glycolate oxidase
748	51	11.1	778	2	E97224	ATP-dependent Lon	821	50.5	11.0	398	2	S75202	hypothetical prote
749	51	11.1	854	2	T23837	hypothetical prote	822	50.5	11.0	399	2	T26257	hypothetical prote
750	51	11.1	862	2	T46289	hypothetical prote	823	50.5	11.0	406	2	T27947	hypothetical prote
751	51	11.1	873	2	T16282	hypothetical prote	824	50.5	11.0	407	2	E70309	hypothetical prote
752	51	11.1	887	2	T01113	translation initia	825	50.5	11.0	408	2	T29949	hypothetical prote
753	51	11.1	967	2	A30325	membrane alanyl am	826	50.5	11.0	410	2	JC7584	basic helix-loop-h
754	51	11.1	1075	2	D70568	hypothetical prote	827	50.5	11.0	411	2	AG3003	conserved hypothet
755	51	11.1	1325	2	A64905	vdek protein - Esc	828	50.5	11.0	411	2	B98280	hypothetical prote
756	51	11.1	1790	1	S27772	vitellogenin precu	829	50.5	11.0	421	2	D70868	probable lipO prot
757	50.5	11.0	137	2	D75337	hypothetical prote	830	50.5	11.0	424	2	A71846	glycinamide ribonu
758	50.5	11.0	141	2	E72580	hypothetical prote	831	50.5	11.0	424	2	B64672	glycinamide ribonu
759	50.5	11.0	155	2	T22027	hypothetical prote	832	50.5	11.0	441	2	AF0411	probable chloride

833	50.5	11.0	442	2	S56057	heavy metal ion re	906	50	10.8	214	2	T10737	extensin-like cell
834	50.5	11.0	448	2	A83775	hypothetical prote	907	50	10.8	216	2	A11441	hypothetical prote
835	50.5	11.0	460	2	G85525	probable deaminase	908	50	10.8	219	2	T38019	uracil phosphoribo
836	50.5	11.0	460	2	E90675	probable deaminase	909	50	10.8	232	2	G protein-coupled	
837	50.5	11.0	470	2	T20851	hypothetical prote	910	50	10.8	236	2	hypothetical prote	
838	50.5	11.0	471	2	D83546	probable amino aci	911	50	10.8	238	2	hypothetical prote	
839	50.5	11.0	474	1	JH0790	lipoprotein lipase	912	50	10.8	250	2	cruxrhodopsin-1 -	
840	50.5	11.0	507	2	T27627	hypothetical prote	913	50	10.8	255	2	probable cobalt AB	
841	50.5	11.0	509	2	G81929	probable iron-upta	914	50	10.8	256	2	probable oxidoredu	
842	50.5	11.0	510	2	T20850	hypothetical prote	915	50	10.8	259	2	oxidoreductase PAB	
843	50.5	11.0	515	2	G75267	ABC transporter, p	916	50	10.8	265	2	hypothetical prote	
844	50.5	11.0	517	2	S21042	cytochrome-c oxida	917	50	10.8	268	2	hypothetical prote	
845	50.5	11.0	518	2	S34565	gene G protein - h	918	50	10.8	274	2	probable binding p	
846	50.5	11.0	518	2	F70831	probable PPG prote	919	50	10.8	282	2	conserved hypotet	
847	50.5	11.0	520	2	AD2383	Na+/H+-exchanging	920	50	10.8	293	2	conserved hypotet	
848	50.5	11.0	526	2	G83436	hypothetical prote	921	50	10.8	295	2	probable integral	
849	50.5	11.0	529	1	YRHU1	monophenol monooxy	922	50	10.8	295	2	transposase - Esch	
850	50.5	11.0	543	2	T37570	WD repeat protein	923	50	10.8	296	2	transposase - Esch	
851	50.5	11.0	543	2	S65462	glucose transport	924	50	10.8	296	2	conserved hypotet	
852	50.5	11.0	544	2	A1979	permease protein o	925	50	10.8	299	2	hypothetical prote	
853	50.5	11.0	545	2	AC1914	hypothetical prote	926	50	10.8	304	2	hypothetical prote	
854	50.5	11.0	546	2	B40407	sterol carrier pro	927	50	10.8	308	2	ubiquinol-cytochro	
855	50.5	11.0	563	2	S32156	mandelonitrile lya	928	50	10.8	314	2	pectinesterase [EC	
856	50.5	11.0	577	2	T52608	probable nitrate t	929	50	10.8	317	2	homoserine kinase	
857	50.5	11.0	584	2	S40013	probable nitrate t	930	50	10.8	332	2	cysteine synthase	
858	50.5	11.0	586	2	F84663	aspartyl-tRNA synt	931	50	10.8	332	2	ferrichrome ABC tr	
859	50.5	11.0	595	2	AD2718	aspartyl-tRNA syn	932	50	10.8	333	2	probable integral	
860	50.5	11.0	595	2	D97500	hypothetical prote	933	50	10.8	337	2	probable semialdeh	
861	50.5	11.0	608	2	S76192	hypothetical prote	934	50	10.8	341	2	cysteine proteinase	
862	50.5	11.0	684	2	T25603	hypothetical prote	935	50	10.8	348	2	dehydrogenase [imp	
863	50.5	11.0	688	2	H96681	protein FlE22.10 l	936	50	10.8	357	2	nicotinate-nucleot	
864	50.5	11.0	704	2	F87706	prolyl oligopeptid	937	50	10.8	357	2	JUN kinase-activat	
865	50.5	11.0	712	2	AD2721	H+ translocating p	938	50	10.8	372	2	para-hydroxybenzoa	
866	50.5	11.0	714	2	H97502	h+ translocating p	939	50	10.8	375	2	hypothetical prote	
867	50.5	11.0	731	2	E82922	phosphate transport	940	50	10.8	380	2	ubiquinol-cytochro	
868	50.5	11.0	736	2	AC2821	bacteriophytochrom	941	50	10.8	388	2	ammonium-transport	
869	50.5	11.0	745	2	C97599	cyanobacterial phy	942	50	10.8	388	2	probable exported	
870	50.5	11.0	819	2	F87708	cell division prot	943	50	10.8	393	2	KRPI protein - yea	
871	50.5	11.0	827	2	A95877	hypothetical prote	944	50	10.8	397	2	probable thymidine	
872	50.5	11.0	908	2	A10327	two-component regu	945	50	10.8	407	2	hypothetical prote	
873	50.5	11.0	942	1	J01674	protein kinase TMK	946	50	10.8	407	2	hypothetical prote	
874	50.5	11.0	962	2	T05845	cell surface glyco	947	50	10.8	414	1	cytochrome P450 Rv	
875	50.5	11.0	1163	1	RWHU1C	hypothetical prote	948	50	10.8	420	2	conserved hypotet	
876	50.5	11.0	1188	2	T20333	structural mainten	949	50	10.8	434	2	hypothetical prote	
877	50.5	11.0	1265	2	T47626	apoptosis associat	950	50	10.8	435	2	D-alanyl-D-alanine	
878	50.5	11.0	1317	2	T33748	capsid protein U57	951	50	10.8	440	1	thymidine phosphor	
879	50.5	11.0	1345	2	T44204	major capsid prote	952	50	10.8	440	1	thymidine phosphor	
880	50.5	11.0	1345	2	T44017	hypothetical prote	953	50	10.8	449	2	Na+-transporting A	
881	50.5	11.0	1400	2	B70963	E2 glycoprotein pr	954	50	10.8	457	1	chromogranin A pre	
882	50.5	11.0	1447	1	VGIHE3	E2 glycoprotein pr	955	50	10.8	457	2	streptogrisin C [E	
883	50.5	11.0	1447	1	VGIHE2	E2 glycoprotein pr	956	50	10.8	460	2	interleukin-6 rece	
884	50.5	11.0	1449	1	A43573	E2 glycoprotein pr	957	50	10.8	473	1	photosystem II chl	
885	50.5	11.0	1459	1	VGIHFS	E2 glycoprotein pr	958	50	10.8	473	1	photosystem II chl	
886	50.5	11.0	1577	2	T15851	hypothetical prote	959	50	10.8	473	2	photosystem II pro	
887	50.5	11.0	1672	2	C81675	polymorphic membra	960	50	10.8	476	2	hypothetical prote	
888	50.5	11.0	1921	2	T13827	kinesin-73 - fruit	961	50	10.8	489	2	multidrug-efflux t	
889	50.5	11.0	89	2	H83795	hypothetical prote	962	50	10.8	494	2	probable cobQ prot	
890	50.5	11.0	100	2	A12298	cobalt transport p	963	50	10.8	498	2	hypothetical prote	
891	50.5	11.0	102	2	A75417	hypothetical prote	964	50	10.8	514	2	potassium channel	
892	50.5	11.0	121	2	B72546	hypothetical prote	965	50	10.8	516	2	Na+-dependent symp	
893	50.5	11.0	138	2	UC1342	phospholipase A2 (	966	50	10.8	532	2	monophenol monooxy	
894	50.5	11.0	147	2	S70109	hypothetical prote	967	50	10.8	533	2	hypothetical prote	
895	50.5	11.0	150	2	G72660	hypothetical prote	968	50	10.8	538	2	probable biotin-de	
896	50.5	11.0	170	2	B66842	NADH2 dehydrogenas	969	50	10.8	538	2	ppg-family protein	
897	50.5	11.0	175	2	T11179	hypothetical prote	970	50	10.8	539	2	cephalosporin acyl	
898	50.5	11.0	175	2	AE1149	outer membrane pro	971	50	10.8	542	2	probable membrane	
899	50.5	11.0	186	2	E82625	BAG-family molecucl	972	50	10.8	545	2	hypothetical prote	
900	50.5	11.0	193	2	T39603	probable periplasm	973	50	10.8	545	2	conserved hypotet	
901	50.5	11.0	203	2	D81934	cryptic protein NM	974	50	10.8	573	2	probable sulfate t	
902	50.5	11.0	203	2	F81171	bacteriorhodopsin-	975	50	10.8	588	2	hypothetical prote	
903	50.5	11.0	211	2	A47686	probable exported	976	50	10.8	598	2	potassium channel	
904	50.5	11.0	211	2	AC0268	ABC transporter, A	977	50	10.8	602	2	potassium channel	
905	50.5	11.0	213	2	G75521		978	50	10.8	602	2	potassium voltage-	

979	50	10.8	606	2	S57552	hypothetical prote	1052	49.5	10.7	400	2	T46383
980	50	10.8	613	2	A56031	potassium channel	1053	49.5	10.7	401	2	D83022
981	50	10.8	614	2	E86194	hypothetical prote	1054	49.5	10.7	403	2	T09322
982	50	10.8	700	2	B81266	DNA topoisomerase	1055	49.5	10.7	424	2	D75330
983	50	10.8	749	1	B39898	phospholipase A2 (	1056	49.5	10.7	427	2	A49518
984	50	10.8	756	2	C84682	hypothetical prote	1057	49.5	10.7	430	1	S32570
985	50	10.8	789	2	AE2688	Na+/H+ antiporter	1058	49.5	10.7	430	2	AF1356
986	50	10.8	789	2	H97469	probable NADH dehy	1059	49.5	10.7	430	2	AG1726
987	50	10.8	810	1	P2WMB8	2a protein - broad	1060	49.5	10.7	432	2	H64383
988	50	10.8	828	2	UC5807	trpJ protein - rat	1061	49.5	10.7	443	2	AE0309
989	50	10.8	835	2	F70363	cation transportin	1062	49.5	10.7	469	2	T34645
990	50	10.8	836	2	C97525	clpA protein (Aur22	1063	49.5	10.7	469	2	S74835
991	50	10.8	836	2	AD2744	ATP-dependent Clp	1064	49.5	10.7	476	1	VNU4R
992	50	10.8	876	2	T07101	lipoxigenase (EC 1	1065	49.5	10.7	476	2	B86829
993	50	10.8	993	2	F97717	hypothetical prote	1066	49.5	10.7	478	2	T33942
994	50	10.8	1015	2	T15830	hypothetical prote	1067	49.5	10.7	502	2	T26256
995	50	10.8	1021	2	A86421	Receptor-like seri	1068	49.5	10.7	505	2	G90419
996	50	10.8	1022	2	F87635	AcRb/Acrp/Acrf fam	1069	49.5	10.7	508	2	H86474
997	50	10.8	1277	2	T14152	synaptic scaffoldi	1070	49.5	10.7	514	2	F87592
998	50	10.8	1338	2	T40993	protein kinase cek	1071	49.5	10.7	524	2	F85429
999	50	10.8	1381	2	T31083	paranodin - rat	1072	49.5	10.7	538	2	T40298
1000	50	10.8	1479	2	T42710	mannose receptor,	1073	49.5	10.7	538	2	A83018
1001	50	10.8	1498	2	B97355	DNA segregation AT	1074	49.5	10.7	552	2	AS1027
1002	50	10.8	1505	2	S26765	genome polyprotein	1075	49.5	10.7	553	2	B90153
1003	50	10.8	1524	2	S68553	surface layer prot	1076	49.5	10.7	556	2	T46842
1004	50	10.8	1526	2	A96528	protein P27J15.14	1077	49.5	10.7	557	2	H97351
1005	50	10.8	1687	2	S41742	calcium channel al	1078	49.5	10.7	559	2	C87307
1006	50	10.8	2109	2	T31352	hypothetical prote	1079	49.5	10.7	566	2	B82173
1007	50	10.8	2819	2	A90551	conserved hypothet	1080	49.5	10.7	579	2	S11027
1008	49.5	10.7	63	2	B90031	hypothetical prote	1081	49.5	10.7	583	2	T48473
1009	49.5	10.7	119	2	PH1544	Ig H chain V regio	1082	49.5	10.7	583	2	B83794
1010	49.5	10.7	130	2	AD2901	hypothetical prote	1083	49.5	10.7	586	1	E69314
1011	49.5	10.7	130	2	S67024	probable membrane	1084	49.5	10.7	660	2	B97853
1012	49.5	10.7	150	2	F87507	conserved hypothet	1085	49.5	10.7	685	2	E71895
1013	49.5	10.7	160	2	C35542	ribosomal protein	1086	49.5	10.7	697	2	T13670
1014	49.5	10.7	165	2	F97676	succinate dehydrog	1087	49.5	10.7	698	2	T12673
1015	49.5	10.7	165	2	S50195	oleosin - rape	1088	49.5	10.7	699	2	T12673
1016	49.5	10.7	171	2	S22194	hypothetical prote	1089	49.5	10.7	700	2	T23629
1017	49.5	10.7	172	2	T39644	apxIC protein - Ac	1090	49.5	10.7	701	2	T13056
1018	49.5	10.7	197	2	A82056	hypothetical prote	1091	49.5	10.7	701	2	T13587
1019	49.5	10.7	214	2	D83881	siderophore (surfa	1092	49.5	10.7	702	2	T13058
1020	49.5	10.7	218	2	AC1253	glycine betaine/ca	1093	49.5	10.7	702	2	T12624
1021	49.5	10.7	218	2	A11615	glycine betaine/ca	1094	49.5	10.7	702	2	T13409
1022	49.5	10.7	226	2	F87449	cell division prot	1095	49.5	10.7	703	2	T13074
1023	49.5	10.7	244	2	E84885	hypothetical prote	1096	49.5	10.7	703	2	T13696
1024	49.5	10.7	251	2	A42281	hypothetical prote	1097	49.5	10.7	706	2	T12748
1025	49.5	10.7	252	1	A34702	amphiregulin precu	1098	49.5	10.7	721	2	F82198
1026	49.5	10.7	255	2	H81302	probable membrane	1099	49.5	10.7	732	2	A83481
1027	49.5	10.7	275	2	H90251	maltoase transport	1100	49.5	10.7	734	1	DERZNS
1028	49.5	10.7	294	2	B83040	ribosomal protein	1101	49.5	10.7	738	2	S58612
1029	49.5	10.7	295	2	T04483	probable ring fing	1102	49.5	10.7	740	2	B84741
1030	49.5	10.7	301	1	S10456	cytochrome c-type	1103	49.5	10.7	745	2	B84673
1031	49.5	10.7	302	2	F83392	hypothetical prote	1104	49.5	10.7	753	2	F69338
1032	49.5	10.7	305	2	A10847	iron transport pro	1105	49.5	10.7	770	2	B56695
1033	49.5	10.7	313	2	AH1672	malonyl CoA-acyl c	1106	49.5	10.7	776	2	S45495
1034	49.5	10.7	315	2	B98226	hypothetical prote	1107	49.5	10.7	788	1	I59282
1035	49.5	10.7	315	2	A23060	conserved hypothet	1108	49.5	10.7	795	2	D82225
1036	49.5	10.7	327	2	T32164	hypothetical prote	1109	49.5	10.7	822	2	T25866
1037	49.5	10.7	328	2	AD1916	alcohol dehydrogen	1110	49.5	10.7	826	2	AC0086
1038	49.5	10.7	330	2	H75353	probable nosx prot	1111	49.5	10.7	850	2	JC5700
1039	49.5	10.7	332	2	T33799	hypothetical prote	1112	49.5	10.7	875	2	T12794
1040	49.5	10.7	334	2	T23444	hypothetical prote	1113	49.5	10.7	888	2	A54280
1041	49.5	10.7	341	2	C98304	probable oligopept	1114	49.5	10.7	914	1	JN0550
1042	49.5	10.7	341	2	AB2979	hypothetical prote	1115	49.5	10.7	945	2	S77052
1043	49.5	10.7	348	2	B48435	cysteine proteinas	1116	49.5	10.7	1039	2	T38447
1044	49.5	10.7	360	2	B87286	conserved hypothet	1117	49.5	10.7	1069	2	D85383
1045	49.5	10.7	367	2	C69500	group II decarboxy	1118	49.5	10.7	1084	2	T15616
1046	49.5	10.7	368	1	CQBEHG	early nuclear anti	1119	49.5	10.7	1121	2	JC7329
1047	49.5	10.7	372	1	D69442	conserved hypothet	1120	49.5	10.7	1132	2	T31107
1048	49.5	10.7	374	1	I39857	spore germination	1121	49.5	10.7	1163	2	A56097
1049	49.5	10.7	374	2	T21513	hypothetical prote	1122	49.5	10.7	1195	2	S76592
1050	49.5	10.7	380	1	TAGB	actinidin (SC 3.4	1123	49.5	10.7	1354	2	AG0538
1051	49.5	10.7	391	2	T43987	pp41, pol processi	1124	49.5	10.7	1461	2	E90696

hypothetical prote  
hypothetical prote  
DNA polymerase pro  
probable beta-lact  
kallicardin precur  
maic protein - Str  
hypothetical prote  
hypothetical prote  
Na+ transporter -  
probable sugar tra  
hypothetical prote  
probable Rieseke ir  
variant surface gl  
multidrug transport  
hypothetical prote  
hypothetical prote  
metabolite permeas  
hypothetical prote  
actin interacting  
membrane transport  
probable sodium/hy  
L-ascorbate oxidas  
2-isopropylmalate  
K+-transporting AT  
K+-transporting AT  
hypothetical prote  
probable ABC trans  
L-ascorbate oxidas  
amino acid transpo  
ABC transporter (A  
replication licens  
NADH2 dehydrogenas  
probable heavy-met  
NADH2 dehydrogenas  
NADH2 dehydrogenas  
hypothetical prote  
NADH2 dehydrogenas  
NADH2 dehydrogenas  
NADH2 dehydrogenas  
NADH2 dehydrogenas  
NADH2 dehydrogenas  
NADH2 dehydrogenas  
probable toxin sec  
probable TonB-depe  
NADH2 dehydrogenas  
NADH2 dehydrogenas  
hypothetical prote  
hypothetical prote  
pyruvate, water di  
transducin-like en  
isp4 protein - fis  
diacylglycerol kin  
phenylalanyl-trNA  
hypothetical prote  
outer membrane uet  
ErbB kinase activa  
hypothetical yomg  
cell differentiat  
iodide peroxidase  
cation-transportin  
tetra-ricopeptide  
hypothetical prote  
hypothetical prote  
WD-repeat protein  
telomerase reverse  
arylphorin-binding  
s-methyltetrahydro  
Rhs-family protein  
hypothetical prote

1125	49.5	10.7	1461	2	A85547	hypothetical prote	1198	49	10.6	355	2	S41686	geranylgeranyltran
1126	49.5	10.7	1492	2	A39322	cystic fibrosis tr	1199	49	10.6	366	2	A64950	membrane-bound pen
1127	49.5	10.7	2150	2	T08165	RNA1 polypeptide	1200	49	10.6	366	2	C85800	probable cytochrom
1128	49.5	10.7	2222	1	A30608	DNA-directed DNA p	1201	49	10.6	366	2	G90951	probable cytochrom
1129	49.5	10.7	2403	2	T30875	PRP8 protein homol	1202	49	10.6	367	2	G96770	hypothetical prote
1130	49.5	10.7	2500	1	WNH052	HIV-EP2 enhancer-b	1203	49	10.6	370	2	AB0602	probable membrane
1131	49.5	10.7	3655	2	T38084	TRAP-like protein	1204	49	10.6	378	2	F64446	chorismate synthas
1132	49	10.6	98	2	T17363	NADH2 dehydrogenas	1205	49	10.6	379	2	E69332	heterodisulfide re
1133	49	10.6	98	2	T17177	NADH2 dehydrogenas	1206	49	10.6	380	2	T11033	ubiquinol-cytochro
1134	49	10.6	129	2	T51182	lsu ribosomal prot	1207	49	10.6	382	2	AH2056	hypothetical prote
1135	49	10.6	129	2	T28993	hypothetical prote	1208	49	10.6	385	2	A86227	hypothetical prote
1136	49	10.6	135	2	F86053	hypothetical prote	1209	49	10.6	391	2	T39673	probable mannosylt
1137	49	10.6	135	2	D91207	hypothetical prote	1210	49	10.6	396	2	T35024	probable glucathio
1138	49	10.6	135	2	A65171	ol35 protein - Esc	1211	49	10.6	400	2	C83511	flagellar protein
1139	49	10.6	137	1	JC4877	phospholipase A2 h	1212	49	10.6	404	2	B86962	probable secreted
1140	49	10.6	140	2	S74898	hypothetical prote	1213	49	10.6	408	2	A37813	Ubp-N-acetylglucos
1141	49	10.6	146	2	T06471	core protein - gar	1214	49	10.6	411	2	S75327	lysostaphin - Syne
1142	49	10.6	154	2	T71379	probable ATPase, c	1215	49	10.6	419	1	S47692	hypothetical 43.8K
1143	49	10.6	157	2	S18651	variant surface an	1216	49	10.6	419	2	B91169	probable transport
1144	49	10.6	157	2	S58025	probable olfactory	1217	49	10.6	419	2	B86015	probable transport
1145	49	10.6	159	2	S77822	probable phenylala	1218	49	10.6	419	2	G70602	hypothetical prote
1146	49	10.6	160	2	S73261	plastoquinol-plast	1219	49	10.6	425	2	A64977	hypothetical prote
1147	49	10.6	163	2	D71062	hypothetical prote	1220	49	10.6	429	2	B87299	probable pknA prot
1148	49	10.6	166	2	D82909	NADH2 dehydrogenas	1221	49	10.6	431	1	E70899	hypothetical prote
1149	49	10.6	167	2	T11439	hypothetical prote	1222	49	10.6	439	2	D72716	hypothetical prote
1150	49	10.6	167	2	B71523	hypothetical prote	1223	49	10.6	444	2	B82023	probable membrane-
1151	49	10.6	167	2	AB3204	hypothetical prote	1224	49	10.6	444	2	T24076	hypothetical prote
1152	49	10.6	169	2	B75490	hypothetical prote	1225	49	10.6	448	2	A70398	cell division prot
1153	49	10.6	170	2	H71937	3-dehydroquinase d	1226	49	10.6	450	2	E69934	conserved hypothet
1154	49	10.6	170	2	F90050	hypothetical prote	1227	49	10.6	458	2	AC1173	amino acid transpo
1155	49	10.6	172	2	T32259	hypothetical prote	1228	49	10.6	458	2	AD1530	amino acid transpo
1156	49	10.6	174	2	E90637	NADH dehydrogenase	1229	49	10.6	463	2	C86042	probable transport
1157	49	10.6	179	1	ERAD34	early E3 20.1K gly	1230	49	10.6	463	2	B91195	probable transport
1158	49	10.6	181	2	JX0247	serine proteinase	1231	49	10.6	463	2	H65166	probable transport
1159	49	10.6	185	2	T41299	hypothetical metal	1232	49	10.6	466	2	G72603	sodium-glutamate s
1160	49	10.6	195	2	AF2690	conserved hypothet	1233	49	10.6	469	1	AJECQ	nitrate reductase
1161	49	10.6	195	2	B97472	hypothetical prote	1234	49	10.6	469	1	A83356	glutamate-ammonia
1162	49	10.6	196	2	T49023	hypothetical prote	1235	49	10.6	469	2	A83356	hypothetical prote
1163	49	10.6	196	2	G87510	hypothetical prote	1236	49	10.6	469	2	G86074	glutamine syntheta
1164	49	10.6	203	2	E72345	hypothetical prote	1237	49	10.6	469	2	H91227	glutamine syntheta
1165	49	10.6	203	2	T32745	conserved hypothet	1238	49	10.6	473	2	T07548	photosystem II chl
1166	49	10.6	205	2	T14744	probable tellurium	1239	49	10.6	475	2	T06061	probable glutamate
1167	49	10.6	207	2	D75341	hypothetical prote	1240	49	10.6	475	2	T06061	cellulase (EC 3.2.
1168	49	10.6	212	2	AC0074	hypothetical prote	1241	49	10.6	476	2	H96802	probable amino aci
1169	49	10.6	217	2	B90765	hypothetical prote	1242	49	10.6	476	2	H96802	phosphotransferase
1170	49	10.6	224	2	AG1795	hypothetical prote	1243	49	10.6	485	2	G65051	hypothetical prote
1171	49	10.6	236	2	E81406	hypothetical prote	1244	49	10.6	485	2	C91075	hypothetical prote
1172	49	10.6	244	2	S07398	gamma-gliadin B pr	1245	49	10.6	485	2	B85920	ATP-dependent RNA
1173	49	10.6	255	4	S31866	hypothetical prote	1246	49	10.6	491	2	B71957	ATP-dependent RNA
1174	49	10.6	262	2	T48546	transposase all806	1247	49	10.6	492	2	G64550	uroporphyrinogen-I
1175	49	10.6	263	2	AB2559	hypothetical prote	1248	49	10.6	493	2	AC1578	uroporphyrinogen-I
1176	49	10.6	276	2	S73410	transcription regu	1249	49	10.6	495	1	A26396	T-cell surface gly
1177	49	10.6	287	2	E83928	probable binding-p	1250	49	10.6	496	2	F83124	probable transcrip
1178	49	10.6	288	2	AH0247	conserved hypothet	1251	49	10.6	507	2	JG0185	LAT1 protein - hum
1179	49	10.6	300	2	G75436	chemotaxis protein	1252	49	10.6	510	2	S55134	probable membrane
1180	49	10.6	308	1	QRECB	hypothetical prote	1253	49	10.6	515	2	C58892	cytochrome-c oxida
1181	49	10.6	308	2	C85802	chemotaxis protein	1254	49	10.6	516	2	T09949	colicin E1 - Esche
1182	49	10.6	308	2	G90953	hpr serine/threoni	1255	49	10.6	522	1	IKEC1	Hydrogenase-4 comp
1183	49	10.6	308	2	H82936	conserved hypothet	1256	49	10.6	526	2	B65024	hypothetical prote
1184	49	10.6	312	2	F87335	homoserine kinase	1257	49	10.6	535	2	D96586	probable integral
1185	49	10.6	322	2	A12671	homoserine kinase	1258	49	10.6	542	2	C70732	probable dihydroli
1186	49	10.6	322	2	G97453	carboxyl reductase	1259	49	10.6	553	1	H70786	probable alpha-treha
1187	49	10.6	324	1	JC4280	hypothetical prote	1260	49	10.6	555	2	S27163	ucanase [importe
1188	49	10.6	334	2	T16772	arginine N-succiny	1261	49	10.6	557	2	AE3040	hucu gene homolog
1189	49	10.6	334	2	E87448	glyceroldehyde 3-p	1262	49	10.6	563	2	G88245	glutamate transport
1190	49	10.6	335	2	T40292	probable dehydroge	1263	49	10.6	573	2	S28901	bp22 protein - Des
1191	49	10.6	337	1	QRECH3	probable PTS syste	1264	49	10.6	582	2	S22195	scaffolding protei
1192	49	10.6	337	2	C81029	probable PTS syste	1265	49	10.6	586	2	PC6006	BAK5 protein - bov
1193	49	10.6	337	2	D85873	hypothetical prote	1266	49	10.6	597	2	S51212	conserved hypothet
1194	49	10.6	345	2	T28026	hypothetical prote	1267	49	10.6	602	2	E70067	regulatory protein
1195	49	10.6	349	2	C86662	chemokine (C-C) re	1268	49	10.6	605	2	D83007	hypothetical prote
1196	49	10.6	352	2	A43113	protein C05E4.13 (	1269	49	10.6	616	2	AG2957	probable c4-dicarb
1197	49	10.6	353	2	H88939		1270	49	10.6	616	2	G98325	



1371	49	10.6	618	2	F84409	arsenite transport	1344	48.5	10.5	269	2	G87134	enoyl-[ACP] reduct
1372	49	10.6	629	2	S29685	retroviral recepto	1345	48.5	10.5	273	2	JS0172	chlorophyll a/b-bi
1373	49	10.6	642	2	C84934	threonine-tRNA lig	1346	48.5	10.5	276	2	D41044	octopine-binding p
1374	49	10.6	660	2	T09537	xanthophyll epoxid	1347	48.5	10.5	277	2	D64666	glutamine ABC tran
1375	49	10.6	672	2	A65034	Hydrogenase-4 comp	1348	48.5	10.5	278	2	G71849	amino acid ABC tra
1376	49	10.6	672	2	D85891	hydrogenase 4 memb	1349	48.5	10.5	283	2	AB2254	hypothetical prote
1377	49	10.6	672	2	H91046	hydrogenase 4 memb	1350	48.5	10.5	283	2	B86331	F6F9.15 protein -
1378	49	10.6	680	2	T29871	hypothetical prote	1351	48.5	10.5	283	2	D71130	probable oligopept
1379	49	10.6	719	2	S63392	probable membrane	1352	48.5	10.5	290	2	F71167	hypothetical prote
1380	49	10.6	740	2	T03847	Fas-binding protei	1353	48.5	10.5	291	2	F81444	probable integral
1381	49	10.6	748	1	I50699	cytosolic phosphol	1354	48.5	10.5	302	2	A75432	3-hydroxybutyryl-C
1382	49	10.6	784	2	JH0101	apolipoprotein B-1	1355	48.5	10.5	312	2	I40201	mgE protein - Bac
1383	49	10.6	796	2	E87636	TonB-dependent rec	1356	48.5	10.5	318	2	B91177	probable hemin per
1384	49	10.6	799	2	T48690	hypothetical prote	1357	48.5	10.5	330	2	C86023	hypothetical prote
1385	49	10.6	812	2	AG3138	fimbrial usher pro	1358	48.5	10.5	332	2	AC0260	hypothetical phage
1386	49	10.6	812	2	D98149	hypothetical prote	1359	48.5	10.5	334	2	C81794	hypothetical prote
1387	49	10.6	816	2	T21713	hypothetical prote	1360	48.5	10.5	340	2	E83126	ferric enterobacti
1388	49	10.6	839	2	S35319	nucleoporin-intera	1361	48.5	10.5	342	2	E71359	hypothetical prote
1389	49	10.6	862	2	S64821	probable membrane	1362	48.5	10.5	355	2	T47527	hypothetical prote
1390	49	10.6	952	2	E84534	hypothetical prote	1363	48.5	10.5	365	2	F87552	dprA protein [impo
1391	49	10.6	969	2	F71418	hypothetical prote	1364	48.5	10.5	370	2	AE0289	conserved hypotet
1392	49	10.6	975	2	T22788	hypothetical prote	1365	48.5	10.5	372	2	C93371	Ig V-region-like B
1393	49	10.6	976	2	S40697	processing endopro	1366	48.5	10.5	382	2	A10040	probable mechano
1394	49	10.6	1041	2	B81281	probable secreted	1367	48.5	10.5	387	2	H88012	protein K1084.2 [i
1395	49	10.6	1054	2	T30933	chitinase [EC 3.2.	1368	48.5	10.5	388	2	T33908	hypothetical prote
1396	49	10.6	1073	1	OYHUHX	heat-stable entero	1369	48.5	10.5	394	2	AE1940	two-component resp
1397	49	10.6	1086	2	T40354	hypothetical prote	1370	48.5	10.5	398	2	F75417	L-sorbose dehydr
1398	49	10.6	1190	2	T00842	probable histidine	1371	48.5	10.5	400	2	AG1208	cell-division prot
1399	49	10.6	1207	2	T52459	sensory transducti	1372	48.5	10.5	400	2	AB1565	cell-division prot
1300	49	10.6	1230	2	S47466	cellulose 1,4-beta	1373	48.5	10.5	401	2	B72329	hypothetical prote
1301	49	10.6	1265	2	T51314	probable CO-induce	1374	48.5	10.5	406	2	T31778	hypothetical prote
1302	49	10.6	1396	2	S36851	L-shaped tail fibe	1375	48.5	10.5	409	2	B85735	probable membrane
1303	49	10.6	1430	2	AP0351	probable autotrans	1376	48.5	10.5	410	2	C86835	hypothetical prote
1304	49	10.6	1530	2	E82085	glutamate synthase	1377	48.5	10.5	416	2	T02194	probable pectinase
1305	49	10.6	1648	2	F84833	probable SNF2/SWI2	1378	48.5	10.5	421	2	E90883	hypothetical prote
1306	49	10.6	2172	2	T20145	hypothetical prote	1379	48.5	10.5	424	2	T31978	hypothetical prote
1307	49	10.6	3164	1	WMBEH6	UL36 protein - hum	1380	48.5	10.5	425	2	T25873	UDP-N-acetylglucos
1308	48.5	10.5	73	2	D91146	hypothetical prote	1381	48.5	10.5	426	2	B75434	hypothetical prote
1309	48.5	10.5	73	2	H85991	hypothetical prote	1382	48.5	10.5	426	2	T45767	hypothetical prote
1310	48.5	10.5	73	2	E65119	hypothetical prote	1383	48.5	10.5	428	2	JQ1864	hypothetical 47.0K
1311	48.5	10.5	75	2	T45361	hypothetical prote	1384	48.5	10.5	431	2	H70731	probable esterase
1312	48.5	10.5	115	1	SPRBG	substance P gamma	1385	48.5	10.5	436	2	I39973	alkaline serine pr
1313	48.5	10.5	116	2	AD2124	hypothetical prote	1386	48.5	10.5	441	2	H89809	hypothetical prote
1314	48.5	10.5	139	2	G71033	hypothetical prote	1387	48.5	10.5	443	2	H70430	K+ transport prote
1315	48.5	10.5	146	1	A47481	interleukin-13 pre	1388	48.5	10.5	461	2	C98120	glycerol-3-phospha
1316	48.5	10.5	165	2	A31635	neural cell adhesi	1389	48.5	10.5	463	2	E81141	xanthine/uracil pe
1317	48.5	10.5	171	2	JE0153	mitochondrial inne	1390	48.5	10.5	467	2	T32292	hypothetical prote
1318	48.5	10.5	180	2	T40562	hypothetical 20.1K	1391	48.5	10.5	470	1	P2WL39	L2 protein - human
1319	48.5	10.5	183	2	B81237	hypothetical prote	1392	48.5	10.5	473	2	T17260	hypothetical prote
1320	48.5	10.5	183	2	G82008	probable integral	1393	48.5	10.5	475	2	T08753	hypothetical prote
1321	48.5	10.5	193	2	C97891	hypothetical prote	1394	48.5	10.5	478	2	D64895	probable membrane
1322	48.5	10.5	198	2	S75989	endopeptidase clp	1395	48.5	10.5	500	2	AD1047	probable amino aci
1323	48.5	10.5	199	2	T38524	ATP synthase subun	1396	48.5	10.5	509	2	A96563	probable protein k
1324	48.5	10.5	199	2	A69859	hypothetical prote	1397	48.5	10.5	510	2	B72007	conserved hypotet
1325	48.5	10.5	208	2	C89697	protein K02B9.4 [i	1398	48.5	10.5	511	2	H90439	hypothetical prote
1326	48.5	10.5	211	2	C59091	hypothetical prote	1399	48.5	10.5	518	2	T05196	hypothetical prote
1327	48.5	10.5	217	2	A98196	hypothetical prote	1400	48.5	10.5	528	2	E81186	L-lactate permease
1328	48.5	10.5	221	2	D64907	membrane protein y	1401	48.5	10.5	537	2	A75123	cell fusion glycop
1329	48.5	10.5	225	2	F81977	hypothetical prote	1402	48.5	10.5	546	1	VGNZRK	gene F protein - r
1330	48.5	10.5	225	2	A86043	probable transposa	1403	48.5	10.5	546	2	S47305	hypothetical prote
1331	48.5	10.5	226	2	T23233	hypothetical prote	1404	48.5	10.5	553	2	C84920	hypothetical prote
1332	48.5	10.5	235	2	AC2809	conserved hypotet	1405	48.5	10.5	553	2	T06499	aplysianin A precu
1333	48.5	10.5	235	2	H97587	hypothetical 25.1K	1406	48.5	10.5	556	2	S68408	hypothetical prote
1334	48.5	10.5	241	2	D84138	hypothetical prote	1407	48.5	10.5	559	2	C75286	methy-accepting c
1335	48.5	10.5	243	2	E96010	conserved hypotet	1408	48.5	10.5	578	2	B82204	probable acyl-coAs
1336	48.5	10.5	245	2	E97425	flagellar biosynth	1409	48.5	10.5	583	2	A70723	env polyprotein pr
1337	48.5	10.5	245	2	AE2643	flagellar biosynth	1410	48.5	10.5	584	1	VCM5IA	probable inositol
1338	48.5	10.5	256	2	D86544	NADH (ubiquinone)	1411	48.5	10.5	590	2	C86465	carbon starvation
1339	48.5	10.5	256	2	H72078	probable sodium-tr	1412	48.5	10.5	598	2	A69609	probable protein k
1340	48.5	10.5	257	2	AI2741	conserved hypotet	1413	48.5	10.5	601	2	G96558	sphingomyelin phos
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1343	48.5	10.5	258	2	H70487	cytochrome-c oxida	1416	48.5	10.5	610	2	AI1110	



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1476 48.5 10.5 1920 2 S43721  
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1489 48.5 10.4 113 2 A00397  
1490 48.5 10.4 118 2 F87447

ABC transporter AT  
serine proteinase,  
hypothetical prote  
acetolactate synth  
polyvinyl-alcohol  
hypothetical prote  
DNA topoisomerase  
hypothetical prote  
hypothetical prote  
NADH2 dehydrogenas  
hypothetical prote  
ABC transporter, p  
NADH2 dehydrogenas  
NADH2 dehydrogenas  
NADH2 dehydrogenas  
NADH2 dehydrogenas  
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NADH2 dehydrogenas  
NADH2 dehydrogenas  
NADH2 dehydrogenas  
neural cell adhesi  
hypothetical prote  
chloride channel p  
probable receptor-  
probable transcrip  
probable DNA prima  
phenylalanine-PRNA  
alpha replication  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
SVGI protein - yea  
potassium channel  
hypothetical prote  
protein C34G6.6 [i  
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zinc finger/leucin  
tetraethionate  
conserved hypoteth  
protein-tyrosine-p  
protein T08A9.1 [i  
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probable periplasm  
protein-tyrosine-p  
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WD-40 repeat prote  
protein-tyrosine-p  
lactocoeptin [EC 3.4  
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protein-tyrosine-p  
lactase [EC 3.2.1.  
lactase [EC 3.2.1.  
beta-glycosidase c  
lactocoeptin [EC 3.4  
homeotic protein c  
genome polyprotein  
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hypothetical prote

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1499 48 10.4 183 2 T37965  
1500 48 10.4 189 2 T34657

## ALIGNMENTS

## RESULT 1

I59391

transmembrane protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C:Accession: I59391

R:Attali, B.; Latter, H.; Rachamim, N.; Garty, H.

Proc. Natl. Acad. Sci. U.S.A. 92, 6092-6096, 1995

A:Title: A corticosteroid-induced gene expressing an 'Isk-like' K+ channel activity in &gt;

A:Reference number: I59391; MUID:95320221; PMID:7597086

A:Accession: I59391

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-87 &lt;RES&gt;

A:Cross-references: UNIPROT:Q63113; UNIPARC:UPI000012ADF7; GB:L41254; NID:g951422; PIDN:

C:Genetics:

A:Gene: 3D CHIF

## Query Match

55.6%; Score 256.5; DB 2; Length 87;

Best Local Similarity 61.5%; Pred. No. 2.8e-21;

Matches 56; Conservative 11; Mismatches 17; Indels 7; Gaps 4;

Qy 1 MERVTLA-LLLAGLTALALENDPFANKDDPFYDWKNLQSLGICGGLAAGIAAVLSG 59

Db 1 MEGITCAFLVVLVAGLPVLEANGP-VDKGSPFYDWESLQLGMIFFGGLLCIAGIAAVLSG 59

Qy 60 KCKYKSSQKQKSP--VPEKAIPILITPGSATT 88

Db 60 KCK--CERNHTPSSLPEKVTPLITPGSAST 87

## RESULT 2

S61552

mammary tumor protein mat8 precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C:Accession: S61552; I48648

R:Morrison, B.W.; Leder, P.

Oncogene 9, 3417-3426, 1994

A:Title: new and ras initiate murine mammary tumors that share genetic markers generally;

A:Reference number: I48271; MUID:95060797; PMID:7970700

A:Accession: S61552

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-88 &lt;MOR&gt;

A:Cross-references: UNIPROT:Q61835; UNIPARC:UPI00002114E; EMBL:X93038; NID:g1085067; P:

C:Genetics:

A:Gene: mat8

F:1-20/Domain: signal sequence #status predicted &lt;SIG&gt;

F:21-88/Product: mammary tumor protein mat8 #status predicted &lt;MAT&gt;

Query Match 52.4%; Score 241.5; DB 2; Length 88;

Best Local Similarity 57.8%; Pred. No. 1.3e-19;

Matches 52; Conservative 11; Mismatches 24; Indels 3; Gaps 3;

Qy 1 MERVTLA-LLLAGLTALALENDPFANKDDPFYDWKNLQSLGICGGLAAGIAAVLSG 59

Db 1 MERVTLA-LLLAGLTALALENDPFANKDDPFYDWKNLQSLGICGGLAAGIAAVLSG 59

Db 1 MOEVLVSLVLLAGLFTLDANDP-ENKNDPPFYDWYSLRVGGLICAGILCALGIIVLMSG 59  
Qy 60 KCKYKSSQKQHPVPEKAIPITPGSATTC 89  
Db 60 KCKCKFKRKP-SHRPGEGPLITPGSAHNC 88  
RESULT 3  
A55571  
Chloride conductance inducer Mat-8 - human  
C;Species: Homo sapiens (man)  
C;Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 09-Jul-2004  
C;Accession: A55571  
R;Morrison, B.W.; Moorman, J.R.; Kowdley, G.C.; Kobayashi, Y.M.; Jones, L.R.; Leder, P.  
J. Biol. Chem. 270, 2176-2182, 1995  
A;Title: Mat-8, a novel phospholeman-like protein expressed in human breast tumors, and  
A;Reference number: A55571; MUID:95138184; PMID:7836447  
A;Accession: A55571  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-87 <MOR>  
A;Cross-references: UNIPROT:Q14802; UNIPARC:UPI0000052765; GB:X93036; GB:S74645; NID:910  
C;Keywords: transmembrane protein  
Query Match 46.5%; Score 214.5; DB 2; Length 87;  
Best Local Similarity 54.5%; Pred. No. 1.2e-16;  
Matches 48; Conservative 11; Mismatches 24; Indels 5; Gaps 4;  
Qy 1 MERVTLALL-LAGTALRANDPPYDWKNLQSLGICGGLAAGTAAVLGSG 59  
Db 1 MQKVTGLLVLAGFPVLDAND-LEDKNSPFYDWHSLQVGLGICAGVLCAMGIIVMSA 59  
Qy 60 KCKYKSSQKQ-HSPVPEKAIPITPGSA 86  
Db 60 KCKCKFGQXSGHH--PGETPPLITPGSA 85  
RESULT 4  
A40533  
CAMP-dependent protein kinase major membrane substrate precursor - dog  
C;Species: Canis lupus familiaris (dog)  
C;Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 09-Jul-2004  
C;Accession: A40533  
R;Palmer, C.J.; Scott, B.T.; Jones, L.R.  
J. Biol. Chem. 266, 11126-11130, 1991  
A;Title: Purification and complete sequence determination of the major plasma membrane s  
A;Reference number: A40533; MUID:91250422; PMID:1710217  
A;Accession: A40533  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-92 <PAL>  
A;Cross-references: UNIPROT:P56513; UNIPARC:UPI0000131C15; GB:M63934  
Query Match 27.4%; Score 126.5; DB 2; Length 92;  
Best Local Similarity 41.4%; Pred. No. 7.1e-07;  
Matches 29; Conservative 15; Mismatches 23; Indels 3; Gaps 2;  
Qy 8 LLLLAG-LTALRANDPPYDWKNLQSLGICGGLAAGTAAVLGSKYKSS 66  
Db 8 LVLCVGLFTATABAP--QEHDPTFYQSIIGLITAGILFILGLIIVLSRRRCRCFKN 65  
Qy 67 QKHSPVPEK 76  
Db 66 QOQRTGEPDE 75  
RESULT 5  
D46435  
Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 31-Dec-1993 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
C;Accession: D46435; S31525  
R;Mercer, R.W.; Blomstedter, D.; Bliss Jr., D.P.; Collins, J.H.; Forbush III, B.

J. Cell Biol. 121, 579-586, 1993  
A;Title: Molecular cloning and immunological characterization of the gamma polypeptide,  
A;Reference number: A46435; MUID:93252993; PMID:8387529  
A;Accession: D46435  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-58 <MER>  
A;Cross-references: UNIPROT:Q04645; UNIPARC:UPI00001262A7; EMBL:X70059; NID:9396; PIDN:C  
A;Note: the authors translated the codon TTC for residue 25 as Pro  
C;Keywords: hydrolase; transmembrane protein  
Query Match 20.9%; Score 96.5; DB 2; Length 58;  
Best Local Similarity 34.6%; Pred. No. 0.00092;  
Matches 18; Conservative 14; Mismatches 19; Indels 1; Gaps 1;  
Qy 27 DDPFYDWKNLQSLGICGGLAAGTAAVLGSKYKSSQKHSPVPEKAI 78  
Db 8 EDPFYDYETVRNGGLIPALAFIVGLVILSKFRFC-GAKRQHRQIPEDGL 58  
RESULT 6  
A46435  
Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - sheep (fragment)  
N;Alternate names: sodium pump gamma chain; sodium/potassium-dependent ATPase gamma chai  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 22-Nov-1993 #sequence\_revision 05-Dec-1998 #text\_change 09-Jul-2004  
C;Accession: A46435; S31524; A27383  
R;Mercer, R.W.; Blomstedter, D.; Bliss Jr., D.P.; Collins, J.H.; Forbush III, B.  
J. Cell Biol. 121, 579-586, 1993  
A;Title: Molecular cloning and immunological characterization of the gamma polypeptide,  
A;Reference number: A46435; MUID:93252993; PMID:8387529  
A;Accession: A46435  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 6-53 <MER>  
A;Cross-references: UNIPROT:Q04680; UNIPARC:UPI0000017CC97  
A;Experimental source: kidney  
A;Note: sequence inconsistent with the nucleotide translation  
A;Note: sequence extracted from NCBI backbone (NCBIN:131232, NCBI:P:131233)  
R;Mercer, R.W.  
submitted to the EMBL Data Library, December 1992  
A;Description: Cloning and sequencing of gamma subunit of sodium potassium ATPase.  
A;Reference number: S31522  
A;Accession: S31524  
A;Molecule type: mRNA  
A;Residues: 6-19 'F', 21-53 <MEW>  
A;Cross-references: UNIPARC:UPI000016C4B7; EMBL:X70061; NID:91255; PIDN:CAA49665.1; PID:  
R;Collins, J.H.; Leszyk, J.  
Biochemistry 26, 8665-8668, 1987  
A;Title: The "gamma-subunit" of Na,K-ATPase: a small, amphiphilic protein with a unique  
A;Reference number: A27383; MUID:88163544; PMID:2831947  
A;Accession: A27383  
A;Molecule type: protein  
A;Residues: 1-19, 'F', 21-33 <COL>  
A;Cross-references: UNIPARC:UPI000017CC98  
C;Complex: heterotrimer; alpha, beta, and gamma chain  
C;Keywords: heterotrimer; hydrolase; transmembrane protein  
Query Match 20.5%; Score 94.5; DB 2; Length 53;  
Best Local Similarity 34.6%; Pred. No. 0.0014;  
Matches 18; Conservative 14; Mismatches 19; Indels 1; Gaps 1;  
Qy 27 DDPFYDWKNLQSLGICGGLAAGTAAVLGSKYKSSQKHSPVPEKAI 78  
Db 3 EDPFYDYETVRNGGLIPALAFIVGLVILSKFRFC-GAKRQHRQIPEDGL 53  
RESULT 7  
B46435  
Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 31-Dec-1993 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
C;Accession: B46435; S31523





J. Biol. Chem. 267, 8650-8657, 1992

A;Title: Cloning, functional expression, and regulation of two K(+) channels in human T

A;Reference number: A38101; MUID:92235098; PMID:1373731

A;Accession: A38101

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-523 <ATT>

A;Cross-references: UNIPROT:P22001; UNIPARC:UPI000016AB94; GB:M85217; NID:g186664; PIDN:

R;Phillipson, L.H.; Hice, R.E.; Schaefer, K.; Lamendola, J.; Bell, G.I.; Nelson, D.J.; S

Proc. Natl. Acad. Sci. U.S.A. 88, 53-57, 1991

A;Title: Sequence and functional expression in Xenopus oocytes of a human insulinoma and

A;Reference number: A38556; MUID:91095456; PMID:1986382

A;Accession: B38556

A;Molecule type: DNA

A;Residues: 1-19, 'G', 21-36, 'V', 38-60, 'L', 62-90, 'V', 92-337, 'S', 339-418, 'S', 420-457, 'LS', 4

A;Cross-references: UNIPARC:UPI00001779F2; GB:M55515

R;Cai, Y.C.; Osborne, P.B.; North, R.A.; Dooley, D.C.; Douglass, J.

DNA Cell Biol. 11, 163-172, 1992

A;Title: Characterization and functional expression of genomic DNA encoding the human ly

A;Reference number: 152990; MUID:92189730; PMID:1547020

A;Accession: 152990

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-60, 'L', 62-523 <RES>

A;Cross-references: UNIPARC:UPI0000001C29; GB:M38217; NID:g186670; PIDN:AAB88073.1; PID:

C;Genetics:

A;Gene: GDB:KCNA3; HGK5

A;Cross-references: GDB:128079; OMIM:176263

A;Map position: lp21-lp13.3

C;Superfamily: potassium channel protein drk1

C;Keywords: glycoprotein; phosphoprotein; potassium channel; transmembrane protein; volt

Query Match 14.4%; Score 66.5; DB 2; Length 523;

Best Local Similarity 20.1%; Pred. NO. 19;

Matches 30; Conservative 14; Mismatches 36; Indels 69; Gaps 5;

Qy 8 LLLLAGLTALEANDP---FANKDDPF-----YYDWKNLQLSLGGLLAIAGI 53

Db 358 ILFSSAVYFAEADDPFGSGSIDPAFWAVVTMTVTGVDHHPVTIGGKIVGSLCAIAGV 417

Qy 54 AAVL-----SGKCKYKSKQK----- 69

Db 418 LTIALPVPVIVSNFYVHRETEGEEQSYMHVGSQHLSSAEBELRKARSNSTLSKSEY 477

Qy 70 -----HSPVPEKAIPLTGSAATTC 89

Db 478 MVIEEGGMHSAFPQ--TPFKTGNSTATC 504

Search completed: May 12, 2006, 21:24:50

Job time : 108 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 12, 2006, 21:18:59 ; Search time 230 Seconds  
(without alignments)  
273.009 Million cell updates/sec

Title: US-10-063-557-50  
Perfect score: 461  
Sequence: 1 MERVTLALLLALGTALEAN.....HSPVPEKAIPITPGSATTC 89

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : Uniprot 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	461	100.0	89	2 Q6UWZ1_HUMAN	Q6UWZ1 homo sapien
2	452	98.0	89	2 Q7Z4M5_HUMAN	Q7Z4M5 homo sapien
3	450	97.6	89	1 FXYD4_HUMAN	FXYD4 homo sapien
4	276.5	60.0	88	1 FXYD4_MOUSE	Q6D2W0 mus musculus
5	256.5	55.6	87	1 FXYD4_RAT	Q63113 rattus norv
6	241.5	52.4	88	1 FXYD3_MOUSE	Q61835 mus musculus
7	234.5	50.9	88	1 FXYD3_RAT	P59645 rattus norv
8	230.5	50.0	88	1 FXYD3_PIG	Q97797 sus scrofa
9	214.5	46.5	87	1 FXYD3_HUMAN	Q14802 homo sapien
10	214.5	46.5	87	2 Q6IB59_HUMAN	Q6IB59 homo sapien
11	203	44.0	70	2 Q80UV3_MOUSE	Q80UV3 mus musculus
12	129	28.0	92	1 P1M_HUMAN	Q00168 homo sapien
13	127.5	27.7	88	2 QARFZ2_TETNG	QARFZ2 tetraodon n
14	126.5	27.4	92	1 P1M_CANFA	P56513 canis fami
15	124.5	27.0	91	1 FXYD6_RAT	Q91XV6 rattus norv
16	123.5	26.8	94	1 FXYD6_MOUSE	Q6D164 mus musculus
17	119	25.8	100	2 Q5M8E9_XENTR	Q5M8E9 xenopus tro
18	116	25.2	94	2 Q70Q12_SQUAC	Q70Q12 squalus aca
19	115.5	25.1	92	1 P1M_MOUSE	Q9Z239 mus musculus
20	115	24.9	95	1 FXYD6_PONPY	Q9B229 pongo pygma
21	113.5	24.6	95	2 Q6DJF4_XENLA	Q6DJF4 xenopus lae
22	113	24.5	92	1 P1M_RAT	Q08589 rattus norv
23	112.5	24.4	95	1 FXYD6_HUMAN	Q9H0Q3 homo sapien
24	112.5	24.4	95	1 FXYD6_MACFA	Q4R566 macaca fasc
25	110	23.9	95	2 Q5ZMS9_CHICK	Q5ZMS9 gallus gall
26	107.5	23.3	87	2 QARH7_TETNG	QARH7 tetraodon n
27	103.5	22.5	94	2 Q6DJD6_XENLA	Q6DJD6 xenopus lae
28	96.5	20.9	58	1 ATNG_BOVIN	Q04645 bos taurus
29	96	20.8	99	2 Q7SZ52_BRARE	Q7SZ52 brachydanio
30	95.5	20.7	53	1 ATNG_SHEEP	Q04680 ovis aries
31	95.5	20.7	65	2 Q58K79_PIG	Q58K79 sus scrofa

32	94	20.4	178	1 FXYD5_HUMAN	Q96DB9 homo sapien
33	92	20.0	178	1 FXYD5_RAT	P59647 rattus norv
34	92	20.0	178	2 Q6P9W0_RAT	Q6P9W0 rattus norv
35	89	19.3	80	1 FXYD7_HUMAN	P58549 homo sapien
36	85	18.4	80	1 FXYD7_MOUSE	P59648 mus musculus
37	84	18.2	178	2 Q81WS1_HUMAN	Q81WS1 homo sapien
38	83	18.0	66	1 ATNG_HUMAN	P54710 homo sapien
39	83	18.0	80	1 FXYD7_RAT	P59649 rattus norv
40	83	18.0	94	1 FXYD8_HUMAN	P58550 homo sapien
41	82.5	17.9	66	1 ATNG_RAT	Q04679 rattus norv
42	79.5	17.2	142	2 Q6P8R9_MOUSE	Q6P8R9 mus musculus
43	78	16.9	70	1 ATNG_MOUSE	Q04646 mus musculus
44	78	16.9	70	2 Q6ITT2_MOUSE	Q6ITT2 mus musculus
45	77.5	16.8	711	2 Q4NGJ7_9MICC	Q4NGJ7 athrobacte
46	76	16.5	289	2 Q4WU10_ASPEU	Q4WU10 aspergillus
47	75.5	16.4	524	2 Q5LQV1_SILPO	Q5LQV1 silicibacte
48	74	16.1	188	2 Q5LM65_SILPO	Q5LM65 silicibacte
49	74	16.1	208	2 Q4R6E0_MACFA	Q4R6E0 macaca fasc
50	73.5	15.9	64	2 Q6ITT1_MOUSE	Q6ITT1 mus musculus
51	73.5	15.9	82	2 Q6ITT0_MOUSE	Q6ITT0 mus musculus
52	73.5	15.9	196	2 Q9GZE7_CAERL	Q9GZE7 caenorhabdi
53	73.5	15.9	330	2 Q84EY9_ENTCL	Q84EY9 enterobacte
54	73	15.8	201	2 Q7QJ63_ANOGA	Q7QJ63 anopheles 9
55	73	15.8	455	2 Q4IPU0_GIBZE	Q4IPU0 gibberella
56	73	15.8	1132	2 Q83861_9REOV	Q83861 nilaparvata
57	73	15.8	1343	2 Q521Q6_MAGGR	Q521Q6 magnaporthe
58	72	15.6	160	1 PETD_SYNY3	P27589 synecocyst
59	71	15.4	61	1 ATNG_XENLA	Q13001 xenopus lae
60	71	15.4	529	2 Q43355_BACSU	Q43355 bacillus su
61	70.5	15.3	251	2 Q54FJ8_DICDI	Q54FJ8 dictyosteli
62	70.5	15.3	334	2 Q6D644_ERWCT	Q6D644 erwinia car
63	70	15.2	184	1 FXYD5_MOUSE	P97808 mus musculus
64	70	15.2	216	2 Q5ZFS6_PLAMJ	Q5ZFS6 plantago ma
65	69.5	15.1	236	2 Q6GME4_XENLA	Q6GME4 xenopus lae
66	69.5	15.1	268	2 Q4FSL8_9GAMM	Q4FSL8 psychobact
67	69.5	15.1	458	2 Q5KUP7_GEOKA	Q5KUP7 geobacillus
68	69	15.0	150	2 Q8ZCD4_YERPE	Q8ZCD4 yersinia pe
69	69	15.0	150	2 Q668G1_YERPS	Q668G1 yersinia ps
70	69	15.0	157	2 Q8D0V1_YERPE	Q8D0V1 yersinia pe
71	68.5	14.9	339	2 Q9LUK8_ARATH	Q9LUK8 arabidopsis
72	68.5	14.9	340	2 Q94EI9_ARATH	Q94EI9 arabidopsis
73	68.5	14.9	456	2 Q9CL30_PASNU	Q9CL30 pasteurella
74	68.5	14.9	485	2 Q58EK5_BRARE	Q58EK5 brachydanio
75	68.5	14.9	499	2 Q5VHU4_CIOIN	Q5VHU4 ciona intes
76	68.5	14.9	531	2 Q5VHU5_CIOIN	Q5VHU5 ciona intes
77	68	14.8	173	2 Q8HKR3_PPERC	Q8HKR3 arcos sp. k
78	68	14.8	417	2 Q4QD23_LEIMA	Q4QD23 leishmania
79	68	14.8	978	2 Q69SP5_ORYSA	Q69SP5 oryza sativ
80	67.5	14.6	135	1 YCF66_MARPO	Q32616 marchantia
81	67.5	14.6	337	2 Q6L3V4_SOLDE	Q6L3V4 solanum dem
82	67.5	14.6	387	2 Q6YVY7_ORYDA	Q6YVY7 oryza sativ
83	67.5	14.6	664	2 Q75485_HUMAN	Q75485 homo sapien
84	67.5	14.6	664	2 Q8WU17_HUMAN	Q8WU17 homo sapien
85	67.5	14.6	664	2 Q5RBT7_PONPY	Q5RBT7 pongo pygma
86	67	14.5	364	2 Q5ZFS7_PLAMJ	Q5ZFS7 plantago ma
87	67	14.5	390	1 AROC_SULTO	Q96Y94 sulfolobus
88	67	14.5	715	2 Q72E54_DESVH	Q72E54 desulfovibr
89	66.5	14.4	198	2 Q5IVA7_MAGDR	Q5IVA7 magnaporthe
90	66.5	14.4	241	2 Q9K313_STRQO	Q9K313 streptomyce
91	66.5	14.4	329	2 Q6OD39_SOLTU	Q6OD39 solanum tub
92	66.5	14.4	359	1 AROC_CHLPN	Q926M2 chlamydia p
93	66.5	14.4	516	2 Q28656_RABIT	Q28656 oryctolagus
94	66.5	14.4	523	1 KCNA3_HUMAN	Q22001 homo sapien
95	66.5	14.4	546	2 Q5RA50_PONPY	Q5RA50 pongo pygma
96	66.5	14.4	549	2 Q8E9W6_SHEON	Q8E9W6 shewanella
97	66.5	14.4	557	2 Q6P2D3_HUMAN	Q6P2D3 homo sapien
98	66.5	14.4	575	2 Q5VMN2_HUMAN	Q5VMN2 homo sapien
99	66	14.3	139	2 Q5XWNO_SOLTU	Q5XWNO solanum tub
100	66	14.3	446	2 Q97UY7_SULSO	Q97UY7 sulfolobus
101	65.5	14.2	161	2 Q5SN36_CRYNE	Q5SN36 cryptococcu
102	65.5	14.2	161	2 Q5KBG5_CRYNE	Q5KBG5 cryptococcu
103	65.5	14.2	305	2 Q74DY6_GEOSL	Q74DY6 geobacter s
104	65.5	14.2	333	2 Q6L3P2_SOLDE	Q6L3P2 solanum dem

105	65.5	14.2	546	2	Q96NJ9_HUMAN	Q96nj9 homo sapien	178	63	13.7	467	2	Q415B1_GIBZE	Q415b1 gibberella
106	65.5	14.2	546	2	Q86V42_HUMAN	Q86v42 homo sapien	179	63	13.7	468	2	Q9ZVA7_ARATH	Q9zva7 arabidopsis
107	65.5	14.2	582	2	Q8N8P5_HUMAN	Q8n8p5 homo sapien	180	63	13.7	496	2	Q7NBZ8_MYCGA	Q7nbz8 mycoplasma
108	65.5	14.2	1185	2	Q8EG56_SHEON	Q8eg56 shewanella	181	63	13.7	622	2	Q59Q13_CANAL	Q59q13 candida alb
109	65.5	14.2	1278	2	Q8SW90_TETNG	Q8sw90 tetraodon n	182	63	13.7	655	2	Q8KWT9_STRMU	Q8kwt9 streptococc
110	65	14.1	134	2	Q5RI57_BRARE	Q5ri57 brachydanio	183	63	13.7	655	2	Q8DUN3_STRMU	Q8dun3 streptococc
111	65	14.1	327	2	Q9LVG3_ARATH	Q9lvg3 arabidopsis	184	63	13.7	750	2	Q59R09_CANAL	Q59r09 candida alb
112	65	14.1	427	2	Q4U9T1_THEAN	Q4u9t1 theileria a	185	63	13.7	808	2	Q6DD69_XENLA	Q6dd69 xenopus lae
113	65	14.1	469	2	Q9XDX1_MAGMG	Q9xdx1 magnetospir	186	63	13.7	825	2	Q993G5_9CANA	Q993g5 callitrichi
114	65	14.1	582	2	Q5UQ22_MIMIV	Q5uq22 mimivirus.	187	63	13.7	912	2	Q8D4M3_VIBVU	Q8d4m3 vibrio vuln
115	65	14.1	760	2	Q90638_CHICK	Q90638 gallus gall	188	63	13.7	917	2	Q5E8X2_VIBFI	Q5e8x2 vibrio fiesc
116	65	14.1	832	2	Q4SBS0_TETNG	Q4sbs0 tetraodon n	189	63	13.7	923	2	Q9N389_CAEBL	Q9n389 caenorhabdi
117	64.5	14.0	155	2	Q9R126_MOUSE	Q9r126 mus musculu	190	63	13.7	1022	2	Q27779_SCHMA	Q27779 schistosoma
118	64.5	14.0	189	2	Q6CLN8_YARLI	Q6cln8 yarrowia li	191	63	13.7	1411	2	Q5AS38_EMENI	Q5as38 aspergillus
119	64.5	14.0	244	2	Q72EX5_DESVH	Q72ex5 desulfovibr	192	62.5	13.6	146	2	Q81GY1_BACCR	Q81gy1 bacillus ce
120	64.5	14.0	311	2	Q4HB57_9DEIO	Q4hb57 deinococcus	193	62.5	13.6	160	2	Q86FE0_SCHJA	Q86fe0 schistosoma
121	64.5	14.0	312	2	Q7LY12_LISMF	Q7ly12 listeria mo	194	62.5	13.6	163	2	Q73CB6_BACCI	Q73cb6 bacillus ce
122	64.5	14.0	372	2	Q5W334_LEGPL	Q5w334 legionella	195	62.5	13.6	207	2	Q8TBL6_HUMAN	Q8tbl6 homo sapien
123	64.5	14.0	452	2	Q7T165_BRARE	Q7t165 brachydanio	196	62.5	13.6	286	2	Q9B9B3_HUMAN	Q9bb3 homo sapien
124	64.5	14.0	452	2	Q8TZX5_PVRFU	Q8tzx5 pyrococcus	197	62.5	13.6	299	1	COMQ_BACSU	P33690 bacillus su
125	64.5	14.0	455	2	Q86080_RHOSH	Q86080 rhodobacter	198	62.5	13.6	303	2	Q9UNZ3_HUMAN	Q9unz3 homo sapien
126	64.5	14.0	465	2	Q9QEW7_9PARA	Q9qew7 measles vir	199	62.5	13.6	339	2	Q53HB8_HUMAN	Q53hb8 homo sapien
127	64.5	14.0	550	2	Q9QEW9_9PARA	Q9qew9 measles vir	200	62.5	13.6	339	2	Q96BY9_HUMAN	Q96by9 homo sapien
128	64.5	14.0	633	2	Q4SHG0_TETNG	Q4shg0 tetraodon n	201	62.5	13.6	339	2	Q9Y6B3_HUMAN	Q9y6b3 homo sapien
129	64.5	14.0	677	2	Q5GUQ5_XANOR	Q5guq5 xanthomonas	202	62.5	13.6	372	2	Q5ZUY1_LEGPH	Q5zuy1 legionella
130	64.5	14.0	725	2	Q8SY05_DROME	Q8sy05 drosophila	203	62.5	13.6	434	2	Q6HHZ7_BACHK	Q6hhz7 bacillus th
131	64.5	14.0	871	2	Q5A4X3_CANAL	Q5a4x3 candida alb	204	62.5	13.6	444	2	Q81PR7_BACCH	Q81pr7 bacillus an
132	64.5	14.0	920	2	Q6XR97_9BACT	Q6xr97 uncultured	205	62.5	13.6	452	2	Q750E3_ASHGO	Q750e3 ashbya goss
133	64.5	14.0	1750	2	Q4WRV3_ASPFU	Q4wrv3 aspergillus	206	62.5	13.6	504	2	Q7S9U0_NEUCO	Q7s9u0 neurospora
134	64	13.9	186	2	Q4RH75_TETNG	Q4rh75 tetraodon n	207	62.5	13.6	525	2	Q76235_TRYCO	Q76235 trypanosoma
135	64	13.9	250	2	Q7WU64_9THEM	Q7wu64 thermotoga	208	62.5	13.6	525	2	Q9NCZ9_TRYCO	Q9ncz9 trypanosoma
136	64	13.9	303	2	Q4KGC4_PSEFS	Q4kgc4 pseudomonas	209	62.5	13.6	539	2	Q9RD59_STRCO	Q9rd59 streptomyce
137	64	13.9	315	2	Q9LS88_ARATH	Q9ls88 arabidopsis	210	62.5	13.6	557	2	Q7XQW8_ORYSA	Q7xqw8 oryza sativ
138	64	13.9	340	2	Q7ZW35_LEPIC	Q7zw35 leptospira	211	62.5	13.6	580	2	Q5T6S3_HUMAN	Q5t6s3 homo sapien
139	64	13.9	383	2	Q6N5J0_RHOPA	Q6n5j0 rhodopseud	212	62.5	13.6	604	2	Q9VNP7_DROME	Q9vnp7 drosophila
140	64	13.9	436	2	Q86VR7_HUMAN	Q86vr7 homo sapien	213	62.5	13.6	621	2	Q6N038_HUMAN	Q6n038 homo sapien
141	64	13.9	525	1	KCNA3_RAT	P15384 rattus norv	214	62.5	13.6	663	2	Q72PX8_LEPIC	Q72px8 leptospira
142	64	13.9	582	2	Q6K6Z0_ORYSA	Q6k6z0 oryza sativ	215	62.5	13.6	663	2	Q8F6A7_LEPIN	Q8f6a7 leptospira
143	64	13.9	667	2	Q9BJM1_TRISP	Q9bjm1 trichinella	216	62.5	13.6	670	2	Q4SQ15_TETNG	Q4sq15 tetradon n
144	64	13.9	678	2	Q8R9G1_THETN	Q8r9g1 thermoanaer	217	62.5	13.6	685	2	Q8E3J6_SHEON	Q8eej6 shewanella
145	64	13.9	727	2	Q6FIK3_CANGA	Q6fik3 candida gla	218	62.5	13.6	700	2	Q8TG00_ASPFU	Q8tg00 aspergillus
146	64	13.9	804	2	Q75GV0_ORYSA	Q75gv0 oryza sativ	219	62.5	13.6	700	2	Q4WS89_ASPFU	Q4ws89 aspergillus
147	64	13.9	915	2	Q7MG71_VIBVU	Q7mg71 vibrio vuln	220	62.5	13.6	760	2	Q7XNU5_ORYSA	Q7xnu5 oryza sativ
148	64	13.9	1046	2	Q82WK5_NITEU	Q82wk5 nitrosomona	221	62.5	13.6	769	1	KCNC3_MOUSE	Q63959 mus musculu
149	63.5	13.8	241	2	Q5UX90_HALMA	Q5ux90 haloarcula	222	62.5	13.6	850	2	Q65MA9_BACILL	Q65ma9 bacillus li
150	63.5	13.8	309	2	Q7YSPT_LISMO	Q7yspt listeria mo	223	62.5	13.6	910	1	SYLA_NEIMA	Q9jw39 neisseria m
151	63.5	13.8	309	2	Q92A05_LISIN	Q92a05 listeria in	224	62.5	13.6	1048	1	SILA_SALTY	Q9zhc9 salmonella
152	63.5	13.8	318	2	Q4IG61_GIBZE	Q4ig61 gibberella	225	62.5	13.6	1048	2	Q6MXQ0_SERMA	Q6mxq0 serratia ma
153	63.5	13.8	327	2	Q6ZVM5_HUMAN	Q6zvm5 homo sapien	226	62	13.4	150	2	Q893N4_CLOTE	Q893n4 clostridium
154	63.5	13.8	359	2	Q822F8_CHLCV	Q822f8 chlamydophi	227	62	13.4	179	1	DSBB_HAEPU	Q7vkv2 haemophilus
155	63.5	13.8	372	2	Q5X4P4_LEGPA	Q5x4p4 legionella	228	62	13.4	189	2	Q6X9L3_SULIS	Q6x9l3 sulfolobus
156	63.5	13.8	396	2	Q5UVL7_9PEZI	Q5uvl7 cercophora	229	62	13.4	289	2	Q6YVW5_ORYSA	Q6yvw5 oryza sativ
157	63.5	13.8	410	2	Q4LUJ0_9BURK	Q4luj0 burkholderi	230	62	13.4	308	2	Q6LBX8_CAEBL	Q6lbx8 caenorhabdi
158	63.5	13.8	420	2	Q6I568_ORYSA	Q6i568 oryza sativ	231	62	13.4	308	2	Q8BFU1_MOUSE	Q8bfu1 mus muscu
159	63.5	13.8	452	2	Q6FVH0_CANGA	Q6fvh0 candida gla	232	62	13.4	331	2	Q8UC07_AGR75	Q8uc07 agrobacteri
160	63.5	13.8	511	1	KCNC1_HUMAN	P48547 homo sapien	233	62	13.4	393	2	Q7CWG7_AGR75	Q7cwg7 agrobacteri
161	63.5	13.8	511	1	KCNC1_MOUSE	P15398 mus musculu	234	62	13.4	414	2	Q32383_STGR	Q32383 streptomyce
162	63.5	13.8	511	2	Q5BN35_RABIT	Q5bn35 oryctolagus	235	62	13.4	419	2	Q7XTD2_ORYSA	Q7xtd2 oryza sativ
163	63.5	13.8	511	2	Q5BN36_BOVIN	Q5bn36 bos taurus	236	62	13.4	445	2	Q96X94_SULTO	Q96x94 sulfolobus
164	63.5	13.8	521	2	Q4V7K2_XENLA	Q4v7k2 xenopus lae	237	62	13.4	470	2	Q8PHB1_XANAC	Q8phb1 xanthomonas
165	63.5	13.8	550	2	Q9QW8_9PARA	Q9qw8 measles vir	238	62	13.4	489	2	Q65UC0_MANSM	Q65uc0 manheimia
166	63.5	13.8	585	1	KCNC1_RAT	P25122 rattus norv	239	62	13.4	558	2	Q8N1V9_HUMAN	Q8n1v9 homo sapien
167	63.5	13.8	585	2	Q9X5U8_CANFA	Q9x5u8 canis famil	240	62	13.4	577	2	Q9V7C4_DROME	Q9v7c4 drosophila
168	63.5	13.8	620	2	Q7UZAS_MYCBO	Q7uzas mycobacteri	241	62	13.4	581	1	FUR4_SCHPO	Q9v7c4 drosophila
169	63.5	13.8	620	2	Q07239_MYCTU	Q07239 mycobacteri	242	62	13.4	613	2	Q96PR0_HUMAN	Q96pr0 schistosach
170	63.5	13.8	642	2	Q4SZN6_TETNG	Q4szn6 tetraodon n	243	62	13.4	629	2	Q86W09_HUMAN	Q86w09 homo sapien
171	63.5	13.8	725	2	Q4HL36_CAMLA	Q4hl36 campylobact	244	62	13.4	638	2	Q96PR1_HUMAN	Q96pr1 homo sapien
172	63.5	13.8	747	2	Q575Z7_NAIZE	Q575z7 zea mays (m	245	62	13.4	641	2	Q4LE77_HUMAN	Q4le77 homo sapien
173	63	13.7	80	2	Q7NU33_CHRVO	Q7nu33 chromobacte	246	62	13.4	777	2	Q51502_PSEAE	Q51502 pseudomonas
174	63	13.7	125	2	Q5JU33_PYRKO	Q5jj33 pyrococcus	247	62	13.4	862	2	Q6MYC9_ASPFU	Q6myc9 aspergillus
175	63	13.7	201	2	Q5NM50_SYNP6	Q5nm50 synecococc	248	62	13.4	862	2	Q4WS99_ASPFU	Q4ws99 aspergillus
176	63	13.7	378	2	Q7QFQ1_ANOGE	Q7qf1 anopheles g	249	62	13.4	952	2	Q6B268_DEBHA	Q6b268 debaryomyce
177	63	13.7	465	2	Q4PDK1_USTWA	Q4pdk1 ustilago ma	250	62	13.4	1025	2	Q4QGS8_LEIMA	Q4qgs8 leishmania



251	62	1057	2	Q6FTI2	CANGA	Q6fti2	candida gla	324	61	13.2	413	2	Q59KD6	CANAL	Q59kd6	candida alb
252	62	2325	2	Q9N3X8	CAEEL	Q9n3x8	caenorhabdi	325	61	13.2	461	2	Q9S5F6	ECOLI	Q9s5f6	escherichia
253	61.5	134	2	Q6TSM0	BRACI	Q6tsm0	bacillus sp	326	61	13.2	461	2	Q7ACQ0	ECOS7	Q7acq0	escherichia
254	61.5	13.3	178	Q83E78	COXBU	Q83e78	coxella bu	327	61	13.2	463	2	Q9VIR1	PYRAB	Q9vir1	pyrococcus
255	61.5	13.3	180	Q6I514	ORYSA	Q6i514	oryza sativ	328	61	13.2	463	2	Q59471	PYRHO	Q59471	pyrococcus
256	61.5	13.3	206	Q5JEL8	PYRKO	Q5jel8	pyrococcus	329	61	13.2	463	2	Q85337	ECOLI	Q85337	escherichia
257	61.5	13.3	210	Q636E4	BACCZ	Q636e4	bacillus ce	330	61	13.2	463	2	Q7DBF2	ECOS7	Q7dbf2	escherichia
258	61.5	13.3	213	Q8FR74	CORF	Q8fr74	corynebacte	331	61	13.2	484	2	Q5GXAL	XANOR	Q5gxal	xanthomonas
259	61.5	13.3	216	Q4NJU0	SMICC	Q4nju0	arthrobacte	332	61	13.2	488	2	Q5ZIJ6	NOCPA	Q5zlj6	nocardia fa
260	61.5	13.3	216	Q7V8X4	PROMM	Q7v8x4	prochloroco	333	61	13.2	502	2	Q5DAP6	SCHTA	Q5dap6	schistosoma
261	61.5	13.3	260	Q89N10	BRAJA	Q89n10	bradyrhizob	334	61	13.2	520	2	Q9SHZ3	ARATH	Q9shz3	arabidopsis
262	61.5	13.3	262	Q9NB91	AGRIP	Q9nb91	agrotis ips	335	61	13.2	542	2	Q5YVG0	NOCPA	Q5yvg0	nocardia fa
263	61.5	13.3	301	Q55KX5	CRYNE	Q55kx5	cryptococcu	336	61	13.2	568	2	Q61FR3	CAEBR	Q61fr3	caenorhabdi
264	61.5	13.3	301	Q5KAK4	CRYNE	Q5kak4	cryptococcu	337	61	13.2	638	2	Q6MLY6	BDEBA	Q6mly6	bellovibri
265	61.5	13.3	303	Q5R491	PONPY	Q5r491	pongo pygma	338	61	13.2	651	2	Q9DDN7	9TELE	Q9ddn7	apteronotus
266	61.5	13.3	320	Q6LPP1	PHOPR	Q6lpp1	photobacter	339	61	13.2	653	2	Q73TB8	MYCPA	Q73tb8	mycobacteri
267	61.5	13.3	327	Q6MX9	BDEBA	Q6mx9	bellovibri	340	61	13.2	1305	1	TCGAP	MOUSE	Q80yf9	mus muscucu
268	61.5	13.3	342	1	ISIA	SYNY3	synechocyst	341	61	13.2	1526	2	Q55IB7	CRYNE	Q55ib7	cryptococcu
269	61.5	13.3	347	Q6RIJZ	MOUSE	Q6rijz	mus musculus	342	61	13.2	1866	2	Q55IB7	CRYNE	Q55ib7	cryptococcu
270	61.5	13.3	381	Q88VV9	LACPL	Q88vv9	lactobacill	343	60.5	13.1	86	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
271	61.5	13.3	382	Q4Q9N5	LEIMA	Q4q9n5	leistmania	344	60.5	13.1	163	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
272	61.5	13.3	399	Q89MV3	BRAJA	Q89mv3	bradyrhizob	345	60.5	13.1	176	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
273	61.5	13.3	427	Q5WKB5	BACSK	Q5wkb5	bacillus cl	346	60.5	13.1	210	1	Q5GVF6	XANOR	Q5gvf6	xanthomonas
274	61.5	13.3	433	Q9KLT7	CHLPN	Q9klt7	chlamydia p	347	60.5	13.1	210	1	Q5GVF6	XANOR	Q5gvf6	xanthomonas
275	61.5	13.3	433	Q9JS97	CHLPN	Q9js97	chlamydia p	348	60.5	13.1	210	1	Q5GVF6	XANOR	Q5gvf6	xanthomonas
276	61.5	13.3	433	Q9Z748	CHLPN	Q9z748	chlamydia p	349	60.5	13.1	210	1	Q5GVF6	XANOR	Q5gvf6	xanthomonas
277	61.5	13.3	434	Q736Y4	BACCI	Q736y4	bacillus ce	350	60.5	13.1	210	1	Q5GVF6	XANOR	Q5gvf6	xanthomonas
278	61.5	13.3	437	Q8NF56	HUMAN	Q8nf56	homo sapien	351	60.5	13.1	227	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
279	61.5	13.3	445	Q57I33	SALCH	Q57i33	salmonella	352	60.5	13.1	289	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
280	61.5	13.3	445	Q5PKR4	SALPA	Q5pkr4	salmonella	353	60.5	13.1	289	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
281	61.5	13.3	445	Q8Z2L3	SALTI	Q8z2l3	salmonella	354	60.5	13.1	295	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
282	61.5	13.3	445	Q8ZL09	SALTY	Q8zl09	salmonella	355	60.5	13.1	306	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
283	61.5	13.3	458	Q6D860	ERWCT	Q6d860	erwinia car	356	60.5	13.1	312	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
284	61.5	13.3	461	Q4FFN8	9LILI	Q4ffn8	acorus amer	357	60.5	13.1	319	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
285	61.5	13.3	495	Q4SRQ6	TETNG	Q4srq6	tetraodon n	358	60.5	13.1	327	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
286	61.5	13.3	522	Q84DU5	LISIV	Q84du5	listeria iv	359	60.5	13.1	340	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
287	61.5	13.3	523	Q84DU4	LISIV	Q84du4	listeria iv	360	60.5	13.1	340	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
288	61.5	13.3	524	1	P60	LISIV	listeria iv	361	60.5	13.1	354	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
289	61.5	13.3	545	Q9QEW6	9PARA	Q9qew6	measles vir	362	60.5	13.1	354	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
290	61.5	13.3	549	Q9V3U6	DROME	Q9v3u6	drosophila	363	60.5	13.1	366	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
291	61.5	13.3	566	Q73L70	TREDE	Q73l70	treponema d	364	60.5	13.1	372	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
292	61.5	13.3	592	Q9PVD1	XENLA	Q9pvd1	xenopus lae	365	60.5	13.1	384	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
293	61.5	13.3	668	Q8BZU9	MOUSE	Q8bzu9	mus musculus	366	60.5	13.1	463	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
294	61.5	13.3	668	Q7TMV1	MOUSE	Q7tmv1	mus musculus	367	60.5	13.1	463	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
295	61.5	13.3	701	Q4G019	HUMAN	Q4g019	homo sapien	368	60.5	13.1	463	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
296	61.5	13.3	746	Q51KR6	MAGGR	Q51kr6	magnaporthe	369	60.5	13.1	474	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
297	61.5	13.3	805	Q62L28	BURMA	Q62l28	burkholderi	370	60.5	13.1	484	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
298	61.5	13.3	831	Q60XB5	CAEBR	Q60xb5	caenorhabdi	371	60.5	13.1	484	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
299	61.5	13.3	855	Q63TB1	BURPS	Q63tb1	burkholderi	372	60.5	13.1	484	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
300	61.5	13.3	977	Q96RD9	HUMAN	Q96rd9	homo sapien	373	60.5	13.1	516	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
301	61.5	13.3	977	Q5VYK9	HUMAN	Q5vyk9	homo sapien	374	60.5	13.1	516	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
302	61.5	13.3	990	Q6Q4G3	HUMAN	Q6q4g3	homo sapien	375	60.5	13.1	560	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
303	61.5	13.3	1145	Q8GUE7	9LILI	Q8gue7	cymodocea n	376	60.5	13.1	618	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
304	61.5	13.3	1322	Q5AL53	CANAL	Q5als3	candida alb	377	60.5	13.1	638	1	Q5GVF6	XANOR	Q5gvf6	xanthomonas
305	61.5	13.3	1499	Q8YK83	ANASP	Q8yk83	anabaena sp	378	60.5	13.1	658	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
306	61	13.2	100	Q8VEB3	PSESY	Q8veb3	pseudomonas	379	60.5	13.1	726	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
307	61	13.2	139	Q87HL7	VIBPA	Q87hl7	vibrio para	380	60.5	13.1	728	1	Q5GVF6	XANOR	Q5gvf6	xanthomonas
308	61	13.2	157	Q8DV17	STRMU	Q8dv17	streptococc	381	60.5	13.1	728	1	Q5GVF6	XANOR	Q5gvf6	xanthomonas
309	61	13.2	173	Q7Q505	ANOAG	Q7q505	anopheles g	382	60.5	13.1	728	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
310	61	13.2	173	Q6MY22	SERMA	Q6my22	serattia ma	383	60.5	13.1	742	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
311	61	13.2	180	Q81IG6	MOUSE	Q81ig6	mus musculus	384	60.5	13.1	776	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
312	61	13.2	187	Q2H2U1	XENTR	Q2h2u1	xenopus tro	385	60.5	13.1	917	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
313	61	13.2	238	Q5V6G2	HALMA	Q5v6g2	haloarcula	386	60.5	13.1	1030	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
314	61	13.2	268	Q9AB59	CAUCR	Q9ab59	caulobacter	387	60.5	13.1	1155	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
315	61	13.2	272	Q54880	RAT	Q54880	rattus norv	388	60.5	13.1	1285	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
316	61	13.2	302	Q54086	COCER	Q54086	coccycus er	389	60.5	13.1	1285	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
317	61	13.2	320	Q76ZD5	MOUSE	Q76zd5	mus musculus	390	60.5	13.1	1285	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
318	61	13.2	326	1	LET	TREDE	treponema d	391	60.5	13.1	1285	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
319	61	13.2	338	1	LET	TREDE	treponema d	392	60.5	13.1	1285	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
320	61	13.2	355	Q95592	COTJA	Q95592	coturnix co	393	60.5	13.1	1285	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
321	61	13.2	380	Q7PG49	ANOAG	Q7pg49	anopheles g	394	60.5	13.1	1285	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
322	61	13.2	389	Q7L197	CHICK	Q7l197	gallus gall	395	60.5	13.1	1285	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas
323	61	13.2	395	2	Q988F9	RHILO	rhizobium l	396	60.5	13.1	1285	2	Q5GVF6	XANOR	Q5gvf6	xanthomonas



397	60.5	13.1	1285	2	08JUV1_9REOV	08JUV1 avian reov	470	59.5	12.9	579	2	05GTF9_WOLTR	05GTF9 wolbachia s
398	60.5	13.1	1319	2	Q5AYC8_EMENI	Q5AYC8 aspergillus	471	59.5	12.9	579	2	073166_WOLPM	073166 wolbachia p
399	60.5	13.1	1748	2	Q5HGZ5_ASPOR	Q5HGZ5 aspergillus	472	59.5	12.9	624	2	055X46_CRYNE	055X46 cryptococcu
400	60	13.0	71	1	VITB1_XENLA	P19010 xenopus lae	473	59.5	12.9	624	2	042R96_PSESM	042R96 pseudomonas
401	60	13.0	165	2	Q8EPX3_OCEIH	Q8EPX3 oceanobacil	474	59.5	12.9	636	2	087ZAB_PSESM	087ZAB pseudomonas
402	60	13.0	218	2	Q6LTG3_PHOPI	Q6LTG3 photobacter	475	59.5	12.9	636	2	098TW3_XENLA	098TW3 xenopus lae
403	60	13.0	249	2	Q8WM93_BRARE	Q8WM93 brachydanio	476	59.5	12.9	677	2	08PSH8_METWA	08PSH8 methanosarc
404	60	13.0	269	2	Q8YXAO_ANASP	Q8YXAO anabena sp	477	59.5	12.9	715	2	08PSH8_METWA	08PSH8 methanosarc
405	60	13.0	275	2	Q9VLF8_DROME	Q9VLF8 drosophila	478	59.5	12.9	735	2	05E380_VIBF1	05E380 vibrio fisc
406	60	13.0	288	2	Q88100_PSEPK	Q88100 pseudomonas	479	59.5	12.9	778	2	04RVZ3_TETNG	04RVZ3 tetradodon n
407	60	13.0	316	2	Q9VNN1_DROME	Q9VNN1 drosophila	480	59.5	12.9	841	2	08H105_ARATH	08H105 arabidopsis
408	60	13.0	324	2	Q986J3_RHILO	Q986J3 rhizobium l	481	59.5	12.9	841	2	08RWY4_ARATH	08RWY4 arabidopsis
409	60	13.0	325	2	Q7XMF8_ORYSA	Q7XMF8 oryza sativ	482	59.5	12.9	847	2	09SGW2_ARATH	09SGW2 arabidopsis
410	60	13.0	341	1	PAX9_HUMAN	P55771 homo sapien	483	59.5	12.9	894	2	08T043_DROME	08T043 drosophila
411	60	13.0	342	1	PAX9_MOUSE	P47242 mus musculu	484	59.5	12.9	1037	2	09VZ53_DROME	09VZ53 drosophila
412	60	13.0	342	2	Q8BS81_MOUSE	Q8BS81 mus musculu	485	59.5	12.9	1048	2	04NQ40_9DELT	04NQ40 anaeromyxob
413	60	13.0	352	2	Q5DWS5_KARMI	Q5DWS5 karlodinim	486	59.5	12.9	1138	2	012371_9VIRU	012371 laguna negr
414	60	13.0	365	2	Q69135_9GAMA	Q69135 human herpe	487	59.5	12.9	1800	2	0817P5_DICDI	0817P5 dictyosteli
415	60	13.0	369	2	Q6D4F3_ERWCT	Q6D4F3 erwinia car	488	59.5	12.9	1800	2	054PV1_DICDI	054PV1 dictyosteli
416	60	13.0	378	2	Q8AZK9_9GAMA	Q8AZK9 human herpe	489	59	12.8	119	2	09GMW2_PIG	09GMW2 sus scrofa
417	60	13.0	412	2	Q913M4_PSEAE	Q913M4 pseudomonas	490	59	12.8	130	2	08XBD8_ECOS7	08XBD8 escherichia
418	60	13.0	497	1	LMP2_EBV	P13285 Epstein-Bar	491	59	12.8	149	2	088UG2_LACPL	088UG2 lactobacill
419	60	13.0	497	2	Q777H4_9GAMA	Q777H4 human herpe	492	59	12.8	150	2	06D7R0_ERWCT	06D7R0 erwinia car
420	60	13.0	502	2	Q9BGH9_9WAMM	Q9BGH9 tachyglossu	493	59	12.8	155	2	092317_MOUSE	092317 mus musculu
421	60	13.0	518	2	Q9XE01_STRVG	Q9XE01 streptomyce	494	59	12.8	167	2	08W9B3_VOMUR	08W9B3 vomabatur
422	60	13.0	519	2	Q82LQ9_STRAW	Q82LQ9 streptomyce	495	59	12.8	169	2	0744S5_MYCPA	0744S5 mycobacteri
423	60	13.0	524	2	Q7T198_CHICK	Q7T198 gallus gall	496	59	12.8	175	2	079713_FALPE	079713 falco peregr
424	60	13.0	525	1	Q83J01_SHIFL	Q83J01 shigella fl	497	59	12.8	177	2	092AM4_LISIN	092AM4 listeria in
425	60	13.0	538	1	YIEC_ECOLI	P26218 escherichia	498	59	12.8	189	2	06X9K8_SULIS	06X9K8 sulfolobus
426	60	13.0	541	2	Q5KN13_CRYNE	Q5KN13 cryptococcu	499	59	12.8	189	2	06X9L0_SULIS	06X9L0 sulfolobus
427	60	13.0	565	2	Q8VD01_MOUSE	Q8VD01 mus musculu	500	59	12.8	189	2	06X9L1_SULIS	06X9L1 sulfolobus
428	60	13.0	580	2	Q7T195_CHICK	Q7T195 gallus gall	501	59	12.8	189	2	06X9L7_SULIS	06X9L7 sulfolobus
429	60	13.0	605	2	Q7NH08_GLOVI	Q7NH08 gloebacter	502	59	12.8	189	2	06X9M0_SULIS	06X9M0 sulfolobus
430	60	13.0	611	2	Q8BYF6_MOUSE	Q8BYF6 mus muscu	503	59	12.8	215	1	YCHE_ECOLI	YCHE_ECOLI escherichia
431	60	13.0	616	2	Q9YIA2_TRYBB	Q9YIA2 trypanosoma	504	59	12.8	215	2	08FHX1_ECOL6	08FHX1 escherichia
432	60	13.0	616	2	Q581Z5_9RYYP	Q581Z5 trypanosoma	505	59	12.8	215	2	Q83RN1_SHIFL	Q83RN1 shigella fl
433	60	13.0	616	2	Q55268_CRYNE	Q55268 cryptococcu	506	59	12.8	215	2	08XDA5_ECOS7	08XDA5 escherichia
434	60	13.0	793	2	Q94BY0_ARATH	Q94BY0 arabidopsis	507	59	12.8	284	2	0594H3_9SPHN	0594H3 agrobacteri
435	60	13.0	819	1	US6NL_MOUSE	Q80XC3 mus musculu	508	59	12.8	293	1	PUR7_BORBR	07WML1 bordetella
436	60	13.0	876	2	Q4T1T5_AZOVI	Q4T1T5 azotobacter	509	59	12.8	293	1	PUR7_BORBR	07WML1 bordetella
437	60	13.0	1056	2	Q4UWV2_XANCP	Q4UWV2 xanthomonas	510	59	12.8	293	1	PUR7_BORBR	07WML1 bordetella
438	60	13.0	1056	2	Q8P875_XANCP	Q8P875 xanthomonas	511	59	12.8	310	2	Q9A410_CACUR	Q9A410 caulobacter
439	60	13.0	1157	2	Q6BHA0_DEBHA	Q6BHA0 debaryomyce	512	59	12.8	326	2	0577P4_BRUAB	0577P4 brucella ab
440	60	13.0	1187	2	Q4SGR6_TETNG	Q4SGR6 tetradodon n	513	59	12.8	326	2	08FWG7_BRUSU	08FWG7 brucella su
441	60	13.0	5217	1	HTS1_COGCA	Q01886 cochlidiobol	514	59	12.8	326	2	08YBV7_BRUMF	08YBV7 brucella me
442	59.5	12.9	209	2	Q5KMN0_CRYNE	Q5KMN0 cryptococcu	515	59	12.8	345	1	ARGC_BACHK	06HE28 bacillus th
443	59.5	12.9	214	2	Q7N459_PHOIL	Q7N459 photorhabdu	516	59	12.8	345	2	0635F0_BACCH	0635F0 bacillus ce
444	59.5	12.9	216	2	Q9GJG8_SALTR	Q9GJG8 salmo trutt	517	59	12.8	350	2	Q7MQV1_WOLSU	Q7MQV1 wolfinella s
445	59.5	12.9	216	2	Q9GJG9_SALTR	Q9GJG9 salmo trutt	518	59	12.8	356	2	Q7XJY8_ORYSA	Q7XJY8 oryza sativ
446	59.5	12.9	216	2	Q9GJH0_SALTR	Q9GJH0 salmo trutt	519	59	12.8	369	2	Q7QZG4_GIALA	Q7QZG4 giardia lam
447	59.5	12.9	217	2	Q9GJH3_SALTR	Q9GJH3 salmo trutt	520	59	12.8	370	2	Q98F86_RHILO	Q98F86 rhizobium l
448	59.5	12.9	217	2	Q9GJH4_SALTR	Q9GJH4 salmo trutt	521	59	12.8	381	2	Q50WP6_ENTHI	Q50WP6 entamoeba h
449	59.5	12.9	217	2	Q9GJH6_SALTR	Q9GJH6 salmo trutt	522	59	12.8	419	2	Q97VB7_SULSO	Q97VB7 sulfolobus
450	59.5	12.9	217	2	Q9GJH7_SALTR	Q9GJH7 salmo trutt	523	59	12.8	420	2	Q926F0_RHIME	Q926F0 rhizobium m
451	59.5	12.9	223	2	Q6PER5_MOUSE	Q6PER5 mus musculu	524	59	12.8	425	2	Q836T8_ENTFA	Q836T8 enterococc
452	59.5	12.9	228	2	Q4RJQ4_TETNG	Q4RJQ4 tetradodon n	525	59	12.8	447	2	Q605T5_METCA	Q605T5 methylococc
453	59.5	12.9	260	2	Q86AQ7_DICDI	Q86AQ7 dictyosteli	526	59	12.8	448	2	Q7NZN0_CHRV0	Q7NZN0 chromobacte
454	59.5	12.9	267	2	Q9CG47_LACLA	Q9CG47 lactococcu	527	59	12.8	463	2	Q8JHG2_BRARE	Q8JHG2 brachydanio
455	59.5	12.9	298	2	Q9KKR2_VIBCH	Q9KKR2 vibrio chol	528	59	12.8	463	2	Q6PC35_BRARE	Q6PC35 brachydanio
456	59.5	12.9	341	2	Q880A3_PSESM	Q880A3 pseudomonas	529	59	12.8	479	1	NUON2_RHIME	P56911 rhizobium m
457	59.5	12.9	342	2	Q9G5Z0_9SAUR	Q9G5Z0 pseudocalot	530	59	12.8	526	2	Q6X1D5_9RYAB	Q6X1D5 aravan viru
458	59.5	12.9	348	2	Q8XKM0_CLOPE	Q8XKM0 clostridium	531	59	12.8	552	2	Q4IBY1_GIBZE	Q4IBY1 gibberella
459	59.5	12.9	356	2	Q9YMW0_NFVLV	Q9YMW0 lymantria d	532	59	12.8	557	2	Q5R7Q0_PONPY	Q5R7Q0 pongo pygma
460	59.5	12.9	384	2	Q72DS9_DESVH	Q72DS9 desulfovibr	533	59	12.8	558	2	Q92C60_LISIN	Q92C60 listeria in
461	59.5	12.9	385	2	Q4SSP1_TETNG	Q4SSP1 tetradodon n	534	59	12.8	575	2	Q9QUU4_KMUPN	Q9QUU4 rattus sp.
462	59.5	12.9	396	2	Q9U3R3_CABEL	Q9U3R3 caenorhabdi	535	59	12.8	579	2	Q6U666_KLPPN	Q6U666 klebsiella
463	59.5	12.9	397	2	Q8XSK5_FALSO	Q8XSK5 ralstonia s	536	59	12.8	598	2	Q4SUR0_TETNG	Q4SUR0 tetradodon n
464	59.5	12.9	426	2	Q6FUK9_CANGA	Q6FUK9 candida gla	537	59	12.8	611	2	Q8WNQ3_PIG	Q8WNQ3 sus scrofa
465	59.5	12.9	431	2	Q7XTD3_ORYSA	Q7XTD3 oryza sativ	538	59	12.8	623	2	Q53W46_THET8	Q53W46 thermus the
466	59.5	12.9	526	2	Q7VI06_HELHP	Q7VI06 helicobacte	539	59	12.8	653	2	Q5REB6_PONPY	Q5REB6 pongo pygma
467	59.5	12.9	527	1	TH11_TRYBB	Q06221 trypanosoma	540	59	12.8	654	1	KCNA4_MOUSE	Q61433 mus musculu
468	59.5	12.9	527	2	Q26765_9TRYP	Q26765 trypanosoma	541	59	12.8	654	1	KCNA4_MOUSE	Q28527 mustela put
469	59.5	12.9	528	1	TH12_TRYBB	Q09037 trypanosoma	542	59	12.8	654	2	Q8CBF8_MOUSE	Q8CBF8 mus musculu

543	59	12.8	655	1	KNNA4_RAT	P15385 rattus norv	616	58.5	12.7	426	2	069513_MYCLE	069513 mycobacteri
544	59	12.8	660	1	KNNA4_BOVIN	Q05037 bos taurus	617	58.5	12.7	463	2	09CB73_MYCLE	09CB73 mycobacteri
545	59	12.8	661	2	Q4MG6_ORISA	Q84mg6 oryza sativ	618	58.5	12.7	471	2	04S1G4_TETNG	04S1G4 tetraodon n
546	59	12.8	662	2	Q9GLF1_BOVIN	Q9glf1 bos taurus	619	58.5	12.7	482	2	097C94_THEVO	097cf4 thermoplas
547	59	12.8	662	2	Q90W36_COLLI	Q90w36 columba liv	620	58.5	12.7	499	2	04NDZ1_9MICC	04ndz1 arthrobacte
548	59	12.8	662	2	Q9YGX8_CHICK	Q9ygx8 gallus gall	621	58.5	12.7	509	2	058NS5_9TRYP	058ns5 trypanosoma
549	59	12.8	663	2	Q61V02_CAEBR	Q61v02 caenorhabdi	622	58.5	12.7	516	2	084DM1_LISSE	084dm1 listeria ae
550	59	12.8	663	2	Q81G57_XENLA	Q81g57 xenopus lae	623	58.5	12.7	516	2	084DU3_LISSE	084du3 listeria ae
551	59	12.8	697	2	Q81G57_XENLA	Q81g57 xenopus lae	624	58.5	12.7	557	2	08VZE2_ARATH	08vze2 arabidopsis
552	59	12.8	700	2	Q8R4E7_PONPY	Q8r4e7 pongo pygma	625	58.5	12.7	565	2	083DB5_COXBU	083db5 coxiella bu
553	59	12.8	771	2	Q80X33_MOUSE	Q80x33 mus musculus	626	58.5	12.7	587	2	09IA29_ONCMU	09ia29 oncorhynch
554	59	12.8	782	2	Q6LKX8_PROPR	Q6lkx8 photobacter	627	58.5	12.7	633	2	09LMH4_ARATH	09lmh4 arabidopsis
555	59	12.8	787	2	Q5SMW7_ORISA	Q5smw7 oryza sativ	628	58.5	12.7	639	2	04HWM9_GIBZE	04hwm9 gibberella
556	59	12.8	816	2	Q98SV4 ICTPU	Q98sv4 ictalurus p	629	58.5	12.7	652	2	06VTW8_NPVCD	06vtw8 choristoneu
557	59	12.8	855	2	Q7NBT0_MYCGA	Q7nbt0 mycoplasma	630	58.5	12.7	683	2	05CN79_CRYHO	05cn79 cryptospori
558	59	12.8	857	1	KNB1_MOUSE	Q03717 mus musculus	631	58.5	12.7	716	2	058QF6_WHEAT	058qf6 triticum ae
559	59	12.8	857	1	KNB1_RAT	P15387 rattus norv	632	58.5	12.7	716	2	053UC8_WHEAT	053uc8 triticoides
560	59	12.8	857	1	Q8KOD1_MOUSE	Q8kod1 mus musculus	633	58.5	12.7	719	2	089ZN6_BACTN	089zn6 bacteroides
561	59	12.8	858	1	KNB1_HUMAN	Q14721 homo sapien	634	58.5	12.7	726	2	08HTN2_9MAGN	08htn2 ranzania ja
562	59	12.8	858	1	KNB1_PIG	Q18868 sus scrofa	635	58.5	12.7	776	1	SYL_NEIME	08ylt2 neisseria m
563	59	12.8	858	1	KNB1_RABIT	Q9nz19 oryctolagus	636	58.5	12.7	876	1	05FAJ3_NEIG1	05faj3 neisseria g
564	59	12.8	898	2	Q91597_XENLA	Q91592 xenopus lae	637	58.5	12.7	1048	2	05EMD9_ECOTI	05emd9 escherichia
565	59	12.8	907	1	KNB2_RAT	Q63099 rattus norv	638	58.5	12.7	1048	2	06USN9_KUEPN	06usn9 klebsiella
566	59	12.8	911	1	KNB2_HUMAN	Q92953 homo sapien	639	58.5	12.7	1095	2	09C7H5_ARATH	09c7h5 arabidopsis
567	59	12.8	911	1	KNB2_RABIT	Q95111 oryctolagus	640	58.5	12.7	1105	2	05F3N7_CHICK	05f3n7 gallus gall
568	59	12.8	911	2	Q7Z7D0_HUMAN	Q7z7d0 homo sapien	641	58.5	12.7	1189	2	0441S5_9RHIZ	0441s5 agrobacteri
569	59	12.8	936	2	Q4ZHA6_BOVIN	Q4zha6 bos taurus	642	58.5	12.7	1346	2	052GR8_MAGGR	052gr8 magnaporthe
570	59	12.8	971	2	Q6GNW5_XENLA	Q6gnw5 xenopus lae	643	58.5	12.7	1720	2	04FXS8_LEIMA	04fxs8 leishmania
571	59	12.8	971	2	Q5AXB1_EMENI	Q5axb1 aspergillus	644	58.5	12.7	1817	2	09SLC7_9NAMM	09slc7 tachylosteu
572	59	12.8	1078	2	Q4ISZ0_AZOVI	Q4isz0 azotobacter	645	58.5	12.7	2473	2	08T3G9_CAEBL	08t3g9 caenorhabdi
573	59	12.8	1211	2	Q57W28_9TRYP	Q57w28 trypanosoma	646	58.5	12.7	2710	2	001808_CAEBL	001808 caenorhabdi
574	59	12.8	1463	2	Q4P3P5_USTMA	Q4p3p5 ustilago ma	647	58.5	12.7	2712	2	08K7K3_SALTY	08k7k3 salmonella
575	58.5	12.7	133	2	Q8DA24_VIBVU	Q8da24 vibrio vuln	648	58.5	12.7	5359	2	05VKR4_SACER	05vkr4 saccharopol
576	58.5	12.7	153	2	Q7MK55_VIBVU	Q7mk55 vibrio vuln	649	58.5	12.7	6193	2	08KSQ0_STRCP	08ksq0 streptomyce
577	58.5	12.7	169	2	Q7MK55_VIBVU	Q7mk55 vibrio vuln	650	58	12.6	96	2	083E08_COXHU	083e08 coxiella bu
578	58.5	12.7	182	2	Q916C9_PSEAE	Q916c9 pseudomonas	651	58	12.6	104	2	024949_FASHE	024949 fasciolla he
579	58.5	12.7	194	2	Q7QBE9_ANOGA	Q7qbe9 anopheles g	652	58	12.6	114	1	YDGD_BASU	YDGD basillus su
580	58.5	12.7	196	1	CLPP_HELHP	Q7vin7 helicobacte	653	58	12.6	120	2	Q4J5Z8_AZOVI	Q4j5z8 azotobacter
581	58.5	12.7	200	2	Q4TT87_CAEBL	Q4tt87 caenorhabdi	654	58	12.6	175	2	05WAS8_BACSK	05was8 bacillus cl
582	58.5	12.7	207	2	Q852L5_ORISA	Q852l5 oryza sativ	655	58	12.6	177	2	09EUW4_LISIN	09euw4 listeria in
583	58.5	12.7	210	2	Q96XX6_SULTO	Q96xx6 sulfolobus	656	58	12.6	185	2	05FJ65_SALPA	05fj65 salmonella
584	58.5	12.7	221	2	Q4SQX2_TETNG	Q4sqx2 tetraodon n	657	58	12.6	185	2	08Z152_SALTI	08z152 salmonella
585	58.5	12.7	222	2	Q7N7R7_PHOLL	Q7n7r7 photorhabd	658	58	12.6	185	2	08ZK73_SALTY	08zk73 salmonella
586	58.5	12.7	238	2	Q4SDB4_TETNG	Q4sdb4 tetraodon n	659	58	12.6	196	2	09RYZ1_DEIRA	09ryz1 deinococcus
587	58.5	12.7	239	2	Q661B5_BRARE	Q661b5 brachydanio	660	58	12.6	215	2	057NR2_SALCH	057nr2 salmonella
588	58.5	12.7	260	1	NRPN_HUMAN	Q60259 homo sapien	661	58	12.6	215	2	05PCV5_SALPA	05pcv5 salmonella
589	58.5	12.7	260	2	Q81W69_HUMAN	Q81w69 homo sapien	662	58	12.6	215	2	07CQF4_SALTY	07cqf4 salmonella
590	58.5	12.7	265	2	Q88YT6_LACPL	Q88yt6 lactobacill	663	58	12.6	232	2	08XF20_SALTI	08xf20 salmonella
591	58.5	12.7	299	2	Q603A7_METCA	Q603a7 methylococc	664	58	12.6	257	1	DPHB_METUA	DPHB methanococc
592	58.5	12.7	299	2	Q7W0P0_BORPE	Q7w0p0 bordetella	665	58	12.6	263	2	03FP64_ORYSA	03fp64 oryza sativ
593	58.5	12.7	299	2	Q7W3G6_BORPE	Q7w3g6 bordetella	666	58	12.6	277	1	RAFR_PEDPE	RAFR pediococcus
594	58.5	12.7	299	2	Q7WET6_BORBR	Q7wet6 bordetella	667	58	12.6	314	2	06IK08_DROME	06ik08 drosophila
595	58.5	12.7	299	2	Q7NMJ4_CHRVO	Q7nmj4 chromobacte	668	58	12.6	325	2	09ELT9_9VIRU	09elt9 rice grassy
596	58.5	12.7	303	2	Q5XVK9_ARATH	Q5xvk9 arabidopsis	669	58	12.6	331	2	065F35_BACLD	065f35 bacillus li
597	58.5	12.7	321	1	TILS_BORPE	Q7vxk92 bordetella	670	58	12.6	333	2	08N7W6_HUMAN	08n7w6 homo sapien
598	58.5	12.7	328	2	Q6LEX6_PLAF7	Q6lex6 plasmodium	671	58	12.6	344	2	04V1K5_BACZ	04v1k5 bacillus ce
599	58.5	12.7	336	2	Q828R5_STRAW	Q828r5 streptomyce	672	58	12.6	344	2	06AXV5_RAT	06axv5 rattus norv
600	58.5	12.7	340	2	Q8R782_THETN	Q8r782 thermoanaer	673	58	12.6	345	1	ARGC_EACAN	ARGC bacillus an
601	58.5	12.7	344	2	Q4NG06_9MICC	Q4ng06 arthrobacte	674	58	12.6	349	2	07MGC8_VIBVU	07mgc8 vibrio vuln
602	58.5	12.7	352	2	Q5ECR9_CANFA	Q5ecr9 canis fami	675	58	12.6	354	2	095HB3_ANAPL	095hb3 anas platyr
603	58.5	12.7	352	2	Q5KSV8_CANFA	Q5ksv8 canis fami	676	58	12.6	368	2	023311_CAEBL	023311 caenorhabdi
604	58.5	12.7	359	2	Q5LSF2_CHLAB	Q5lsf2 chlamydomo	677	58	12.6	376	2	0926X9_LISIN	0926x9 listeria in
605	58.5	12.7	366	2	Q9RR9_BRAJA	Q9rr9 bradyrhizob	678	58	12.6	383	2	0926X9_LISIN	0926x9 listeria in
606	58.5	12.7	372	2	Q8SGX1_9SAUR	Q8sgx1 pareas macu	679	58	12.6	395	2	031BN5_BACCR	031bn5 bacillus ce
607	58.5	12.7	383	1	FAD6E_ARATH	Q89gxl arabidopsis	680	58	12.6	398	1	07PSF3_ANOGA	07psf3 anopheles g
608	58.5	12.7	383	2	Q8LFX8_ARATH	Q8lfz8 arabidopsis	681	58	12.6	398	1	09KPH1_VIBCH	09kph1 vibrio chol
609	58.5	12.7	385	2	Q8UAR7_AGRT5	Q8uar7 agrobacteri	682	58	12.6	403	2	05F7W0_NEIG1	05f7w0 neisseria g
610	58.5	12.7	389	2	Q5ZLL9_ORYSA	Q5zll9 oryza sativ	683	58	12.6	409	2	04MX56_BACCE	04mx56 bacillus ce
611	58.5	12.7	392	2	Q7CS44_AGRT5	Q7cs44 agrobacteri	684	58	12.6	411	2	07YQP7_OCHPR	07yqp7 ochotona pr
612	58.5	12.7	400	1	Q6C9T8_YARLI	Q6c9t8 yarowia li	685	58	12.6	440	2	Q4MSY3_BACCE	Q4msy3 bacillus ce
613	58.5	12.7	409	2	EFTU_HERAU	P42477 herpetosiph	686	58	12.6	440	2	Q6HKY9_BACHK	Q6hky9 bacillus th
614	58.5	12.7	409	2	Q8DBZ6_VIBVU	Q8dbz6 vibrio vuln	687	58	12.6	440	2	081FL1_BACCR	081fl1 bacillus ce
615	58.5	12.7	411	2	Q8RU03_DEIRA	Q8ru03 deinococcus	688	58	12.6	440	2		
			425	1	YOSB_SCHPO	Q9p712 schizosacch							

689	58	12.6	440	2	Q73AS4	BACCI1	Q73as4	bacillus ce	762	57.5	12.5	388	2	Q54466	STRMY	Q54466	streptomyc
690	58	12.6	440	2	Q63D66	BACCCZ	Q63dg6	bacillus ce	763	57.5	12.5	401	2	Q87427	PODAN	Q87427	podospora a
691	58	12.6	440	2	Q81SQ4	BACAN	Q81sq4	bacillus an	764	57.5	12.5	402	2	Q727Q2	HUMAN	Q727q2	homo sapien
692	58	12.6	444	2	Q4SMG6	TETNG	Q4smg6	tetradodon n	765	57.5	12.5	426	2	Q57137	BETA	Q57137	human herpe
693	58	12.6	448	2	Q84DP2	LISMO	Q84dp2	listeria mo	766	57.5	12.5	433	2	Q4H838	DEIO	Q4h838	deinococcus
694	58	12.6	457	2	Q4KJP7	PSEF5	Q4kjp7	pseudomonas	767	57.5	12.5	441	2	Q60NJ4	CAEBR	Q60nj4	caenorhabdi
695	58	12.6	461	2	Q8ZR07	SALTY	Q8zr07	salmonella	768	57.5	12.5	446	2	Q6H7Q3	ORYSA	Q6h7q3	oryza sativ
696	58	12.6	462	2	Q8RYH5	DEIRA	Q8ryh5	deinococcus	769	57.5	12.5	448	2	Q6NBL7	RHOPE	Q6nbl7	rhodopseudo
697	58	12.6	466	2	Q6DBW3	BRARE	Q6dbw3	brachydanio	770	57.5	12.5	453	2	Q7ZVN2	BRARE	Q7zvn2	brachydanio
698	58	12.6	487	2	Q4T7M0	TETNG	Q4t7m0	tetradodon n	771	57.5	12.5	461	2	Q5PM91	SALPA	Q5pm91	salmonella
699	58	12.6	511	2	Q74CB3	GEOSL	Q74cb3	geobacter s	772	57.5	12.5	461	2	Q8Z815	SALTI	Q8z815	salmonella
700	58	12.6	541	2	Q9Y1L1	LOCM1	Q9y1l1	locusta mig	773	57.5	12.5	461	2	Q916E1	PSEAE	Q916e1	pseudomonas
701	58	12.6	549	2	Q8GGR2	STRAZ	Q8ggr2	streptomyce	774	57.5	12.5	461	2	Q65QV2	MANSM	Q65qv2	mannheimia
702	58	12.6	552	2	Q4J322	AZOV1	Q4j322	azotobacter	775	57.5	12.5	502	2	Q5V1D8	HALMA	Q5v1d8	haloarcula
703	58	12.6	553	2	Q942J6	ORYSA	Q942j6	oryza sativ	776	57.5	12.5	507	2	Q5BPF5	RAT	Q5bpf5	rattus norv
704	58	12.6	614	2	Q7UVX4	RHOBA	Q7uvx4	rhodopirell	777	57.5	12.5	517	2	Q8EV45	MYCPE	Q8ev45	mycoplasma
705	58	12.6	629	2	Q86146	CAMJE	Q86146	campylobact	778	57.5	12.5	523	2	Q916Z6	PSEAE	Q916z6	pseudomonas
706	58	12.6	674	2	Q8PH21	XANAC	Q8ph21	xanthomonas	779	57.5	12.5	528	1	KCNA3	MOUSE	P16390	mus musculus
707	58	12.6	675	2	Q5H226	XANOR	Q5h226	xanthomonas	780	57.5	12.5	531	2	Q8ERG1	OCETH	Q8erg1	oceanobacil
708	58	12.6	676	2	Q8XQP3	RALSO	Q8xqp3	raistonia s	781	57.5	12.5	541	2	Q4SFX1	TETNG	Q4sfx1	tetradodon n
709	58	12.6	681	1	GA2L1	HUMAN	Q9501	homo sapien	782	57.5	12.5	574	2	Q8XQ27	RALSO	Q8xq27	raistonia s
710	58	12.6	682	2	Q4HU14	GIBZE	Q4hu14	gibberella	783	57.5	12.5	581	2	Q6BK68	DEBHA	Q6bk68	debaromyce
711	58	12.6	695	2	Q4HLX6	CAMLA	Q4hlx6	campylobact	784	57.5	12.5	594	2	Q98PX5	MYCPU	Q98px5	mycoplasma
712	58	12.6	743	2	Q6FJV9	CANGA	Q6fjv9	candida gla	785	57.5	12.5	603	2	Q4P4K6	USTWA	Q4p4k6	ustilago ma
713	58	12.6	758	2	Q9VQW0	DROME	Q9vqw0	drosophila	786	57.5	12.5	636	2	Q86486	9PARA	Q86486	rinderpest
714	58	12.6	767	2	Q51CV0	ENTHI	Q5lcvo	entamoeba h	787	57.5	12.5	656	2	Q8K244	MOUSE	Q8k244	mus musculus
715	58	12.6	776	2	Q60ZP1	CAEBR	Q60zpl	caenorhabdi	788	57.5	12.5	662	1	HEPA	HHV6Z	P52451	human herpe
716	58	12.6	782	2	Q91593	XENLA	Q91593	xenopus lae	789	57.5	12.5	662	2	Q9WT01	9BETA	Q9wt01	human herpe
717	58	12.6	786	2	Q5BDP3	EMENI	Q5bdp3	aspergillus	790	57.5	12.5	668	2	Q4UXH5	XANCP	Q4uxh5	xanthomonas
718	58	12.6	1006	2	Q4NI49	GWICC	Q4ni49	arthrobacte	791	57.5	12.5	668	2	Q8P6N7	XANCP	Q8p6n7	xanthomonas
719	58	12.6	1018	2	Q6ALX0	DESPS	Q6alx0	desulfotale	792	57.5	12.5	670	2	Q9BAQ4	9MAGN	Q9baq4	buxus citri
720	58	12.6	1051	2	Q5B9V4	EMENI	Q5b9v4	aspergillus	793	57.5	12.5	671	2	Q5AKV5	CANAL	Q5akv5	candida alb
721	58	12.6	1056	2	Q7S9Q2	NEUCR	Q7s9q2	neurospora	794	57.5	12.5	682	2	Q9BAR1	9MAGN	Q9bar1	buxus glome
722	58	12.6	1056	2	Q8PJN1	XANAC	Q8pjn1	xanthomonas	795	57.5	12.5	745	1	FURL	HELHP	Q519G2	haemobacte
723	58	12.6	1109	2	Q7JRS2	DROME	Q7jr52	drosophila	796	57.5	12.5	750	2	Q617U6	CAEBR	Q617u6	caenorhabdi
724	58	12.6	1135	2	Q9VTE8	DROSOPHILA	Q9vte8	drosophila	797	57.5	12.5	771	2	Q75JP4	DICD1	Q75jp4	dictyosteli
725	58	12.6	1149	2	Q7KUB4	DROME	Q7kue4	drosophila	798	57.5	12.5	772	2	Q6GP40	XENLA	Q6gp40	xenopus lae
726	58	12.6	1821	2	Q7PQ11	ANOQA	Q7pq11	anopheles g	799	57.5	12.5	794	2	Q8IQN2	DROME	Q8iqn2	drosophila
727	58	12.6	1905	2	Q8XTF6	FLABE	Q8xtf6	plasmodium	800	57.5	12.5	822	2	Q8IQN2	DROME	Q8iqn2	drosophila
728	58	12.6	2576	2	Q8JFV5	BRARE	Q8jfv5	brachydanio	801	57.5	12.5	857	1	QFQH	PSEPK	Q88D04	pseudomonas
729	58	12.6	4836	2	Q4U2R1	MOUSE	Q4u2r1	mus musculus	802	57.5	12.5	865	2	Q61J98	CAEBR	Q61j98	caenorhabdi
730	58	12.6	4836	2	Q88473	MOUSE	Q88473	mus musculus	803	57.5	12.5	882	2	Q8MQK2	DROME	Q8mqk2	drosophila
731	57.5	12.5	71	1	VITB2	XENLA	P19011	xenopus lae	804	57.5	12.5	907	2	Q8VY10	ARATH	Q8vy10	arabidopsis
732	57.5	12.5	84	2	Q8T6F5	DROPS	Q8t6f5	drosophila	805	57.5	12.5	1012	2	Q8XUM5	RALSO	Q8xum5	raistonia s
733	57.5	12.5	128	2	Q9NG36	WAMER	Q9ng36	mamestra br	806	57.5	12.5	1071	2	Q933P2	9GANA	Q933p2	calitrichi
734	57.5	12.5	129	2	Q4K8V9	PSEF5	Q4k8v9	pseudomonas	807	57.5	12.5	1625	2	Q6MVD4	NEUCR	Q6mvd4	neurospora
735	57.5	12.5	139	2	Q8Z6V7	SALTI	Q8z6v7	salmonella	808	57.5	12.5	1681	2	Q4SVT8	TETNG	Q4svt8	tetradodon n
736	57.5	12.5	144	2	Q5YXC3	NOCFA	Q5yxc3	nocardia fa	809	57.5	12.5	1696	2	Q4NOK7	THEPA	Q4nok7	theileria p
737	57.5	12.5	144	2	Q9ERF0	RAT	Q9erf0	rattus norv	810	57.5	12.5	1751	2	Q57V95	9TRYP	Q57v95	trypanosoma
738	57.5	12.5	146	2	Q5LS51	SILPO	Q5ls51	silicibacte	811	57.5	12.5	1902	1	P2P	LACPA	Q02470	lactobacill
739	57.5	12.5	153	2	Q8K071	MOUSE	Q8k071	mus musculus	812	57.5	12.5	2235	1	CHD7	HUMAN	Q9p2d1	homo sapien
740	57.5	12.5	173	2	Q85CX0	STELE	Q85cx0	salangichth	813	57.5	12.5	2322	2	Q60ZNS	CAEBR	Q60zns	caenorhabdi
741	57.5	12.5	184	2	Q5U4U5	XENLA	Q5u4u5	xenopus lae	814	57.5	12.5	3300	2	Q4NI27	THEPA	Q4ni27	theileria p
742	57.5	12.5	194	2	Q5BIN4	BOVIN	Q5bin4	bos taurus	815	57.5	12.5	105	2	Q4FTI0	9GAMM	Q4fti0	psychroba
743	57.5	12.5	224	1	CLPPI	SYNPK	Q7ua36	synecococc	816	57.5	12.4	148	2	Q9ZV24	ARATH	Q9zlv24	arabidopsis
744	57.5	12.5	245	2	Q83T33	SALTI	Q83t33	salmonella	817	57.5	12.4	148	2	Q8E595	STRA3	Q8e595	stretococc
745	57.5	12.5	252	2	Q7XQ06	ORYSA	Q7xq06	oryza sativ	818	57.5	12.4	148	2	Q6F8W5	CANGA	Q6f8w5	candida gla
746	57.5	12.5	292	2	Q6FUC0	CANGA	Q6fuc0	candida gla	819	57.5	12.4	158	2	Q6F8W5	CANGA	Q6f8w5	candida gla
747	57.5	12.5	307	2	Q46720	ECOLI	Q46720	escherichia	820	57.5	12.4	166	2	Q6F8W5	CANGA	Q6f8w5	candida gla
748	57.5	12.5	313	2	Q7NWF7	CHRW0	Q7nwf7	chromobacte	821	57.5	12.4	171	2	Q5LKW5	SILPO	Q5lkw5	schistosoma
749	57.5	12.5	323	2	Q93H09	STRAW	Q93h09	streptomyce	822	57.5	12.4	177	2	Q8L827	ARATH	Q8l827	arabidopsis
750	57.5	12.5	324	2	Q9S248	STRCO	Q9s248	streptomyce	823	57.5	12.4	184	2	Q4TMQ7	9SPHN	Q4tmq7	erythroba
751	57.5	12.5	337	2	Q817B2	FASHE	Q817b2	fasciola he	824	57.5	12.4	184	2	Q4TMQ7	9SPHN	Q4tmq7	erythroba
752	57.5	12.5	342	1	ISIA	SYNPK	P11157	synecococc	825	57.5	12.4	185	1	ADML	RAT	P33145	rattus norv
753	57.5	12.5	353	2	Q91R55	ARATH	Q91r55	arabidopsis	826	57.5	12.4	190	1	PYRE	THETN	P58858	thermoanaer
754	57.5	12.5	355	2	Q4JFC3	MOUSE	Q4jfc3	mus musculus	827	57.5	12.4	228	2	Q83TM7	LISMO	Q83tm7	listeria mo
755	57.5	12.5	356	2	Q9Y941	AEERPE	Q9y941	aeropyrum p	828	57.5	12.4	230	2	Q8EG49	SHEON	Q8eg49	shewanella
756	57.5	12.5	363	2	Q6D013	ERWCT	Q6d013	erwinia car	829	57.5	12.4	241	2	Q658A8	ORYSA	Q658a8	oryza sativ
757	57.5	12.5	371	2	Q53GK2	HUMAN	Q53gk2	homo sapien	830	57.5	12.4	254	2	Q61095	TRYCR	Q61095	trypanosoma
758	57.5	12.5	371	2	Q9J8C7	SPNOCL	Q9j8c7	spodoptera	831	57.5	12.4	258	1	UDP	TREPA	Q03990	uncultured
759	57.5	12.5	374	1	OE56	NPVOP	Q83953	orgyia pseu	832	57.5	12.4	268	2	Q70FH9	9CYAN	Q70fh9	9cyano
760	57.5	12.5	379	1	MCP	CAVOP	P70105	cavia porce	833	57.5	12.4	269	2	Q8YQW0	ANASP	Q8yqw0	anabaena sp
761	57.5	12.5	383	2	Q8A166	BACTIN	Q8a166	bacteroides	834	57.5	12.4	276	2	Q68ES3	XENLA	Q68es3	xenopus lae

835	57	12.4	283	2	Q4V7U2_XENLA	Q4V7u2 xenopus lae	908	57	12.4	811	2	Q4FXZ2_LEIMA	Q4fxz2 leishmania
836	57	12.4	291	2	Q5WX66_LEGPL	Q5wx66 legionella	909	57	12.4	858	2	Q6ZPE7_MOUSE	Q6zpe7 mus musculus
837	57	12.4	292	2	Q6UY47_HUMAN	Q6uy47 homo sapien	910	57	12.4	880	2	Q6K107_MYCNO	Q6k107 mycoplasma
838	57	12.4	301	2	Q8BYJ2_MOUSE	Q8byj2 mus musculus	911	57	12.4	892	2	Q5LUM8_SILPO	Q5lum8 silicibacte
839	57	12.4	302	2	Q768S4_MOUSE	Q768s4 mus musculus	912	57	12.4	1056	1	Q5LUM8_SILPO	Q5lum8 silicibacte
840	57	12.4	315	2	Q768S4_MOUSE	Q768s4 mus musculus	913	57	12.4	1056	1	Q5LUM8_SILPO	Q5lum8 silicibacte
841	57	12.4	325	2	Q9UN22_HUMAN	Q9une2 homo sapien	914	57	12.4	1137	2	Q5LUM8_SILPO	Q5lum8 silicibacte
842	57	12.4	325	2	Q9UN22_HUMAN	Q9une2 homo sapien	915	57	12.4	1137	2	Q5LUM8_SILPO	Q5lum8 silicibacte
843	57	12.4	332	2	Q52M67_PAVLU	Q52m67 pavlova lut	916	57	12.4	1294	2	Q52M67_PAVLU	Q52m67 pavlova lut
844	57	12.4	334	2	Q2W833_BANAT	Q2w833 bangia atro	917	57	12.4	1491	2	Q52M67_PAVLU	Q52m67 pavlova lut
845	57	12.4	342	1	ISIA_SYN7P	P15347 synechococc	918	57	12.4	1574	2	Q52M67_PAVLU	Q52m67 pavlova lut
846	57	12.4	342	2	Q5N675_SYN6P	Q5n675 synechococc	919	57	12.4	1639	2	Q52M67_PAVLU	Q52m67 pavlova lut
847	57	12.4	343	2	Q5LMS6_SILPO	Q5lms6 silicibacte	920	57	12.4	1875	2	Q5LMS6_SILPO	Q5lms6 silicibacte
848	57	12.4	351	2	Q5LMS6_SILPO	Q5lms6 silicibacte	921	57	12.4	2660	2	Q5LMS6_SILPO	Q5lms6 silicibacte
849	57	12.4	352	2	Q5LMS6_SILPO	Q5lms6 silicibacte	922	57	12.4	3196	2	Q5LMS6_SILPO	Q5lms6 silicibacte
850	57	12.4	353	2	Q5LMS6_SILPO	Q5lms6 silicibacte	923	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
851	57	12.4	355	2	Q5LMS6_SILPO	Q5lms6 silicibacte	924	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
852	57	12.4	360	2	Q5LMS6_SILPO	Q5lms6 silicibacte	925	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
853	57	12.4	374	2	Q5LMS6_SILPO	Q5lms6 silicibacte	926	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
854	57	12.4	374	2	Q5LMS6_SILPO	Q5lms6 silicibacte	927	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
855	57	12.4	374	2	Q5LMS6_SILPO	Q5lms6 silicibacte	928	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
856	57	12.4	376	2	Q5LMS6_SILPO	Q5lms6 silicibacte	929	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
857	57	12.4	383	2	Q5LMS6_SILPO	Q5lms6 silicibacte	930	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
858	57	12.4	383	2	Q5LMS6_SILPO	Q5lms6 silicibacte	931	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
859	57	12.4	384	2	Q5LMS6_SILPO	Q5lms6 silicibacte	932	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
860	57	12.4	385	2	Q5LMS6_SILPO	Q5lms6 silicibacte	933	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
861	57	12.4	386	2	Q5LMS6_SILPO	Q5lms6 silicibacte	934	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
862	57	12.4	387	2	Q5LMS6_SILPO	Q5lms6 silicibacte	935	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
863	57	12.4	387	2	Q5LMS6_SILPO	Q5lms6 silicibacte	936	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
864	57	12.4	399	2	Q5LMS6_SILPO	Q5lms6 silicibacte	937	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
865	57	12.4	409	2	Q5LMS6_SILPO	Q5lms6 silicibacte	938	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
866	57	12.4	425	2	Q5LMS6_SILPO	Q5lms6 silicibacte	939	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
867	57	12.4	440	2	Q5LMS6_SILPO	Q5lms6 silicibacte	940	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
868	57	12.4	440	2	Q5LMS6_SILPO	Q5lms6 silicibacte	941	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
869	57	12.4	456	2	Q5LMS6_SILPO	Q5lms6 silicibacte	942	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
870	57	12.4	457	1	PROY_EC0LI	Q5lms6 silicibacte	943	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
871	57	12.4	457	1	PROY_EC0LI	Q5lms6 silicibacte	944	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
872	57	12.4	461	1	DCUC_EC0LI	Q5lms6 silicibacte	945	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
873	57	12.4	461	2	Q5LMS6_SILPO	Q5lms6 silicibacte	946	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
874	57	12.4	461	2	Q5LMS6_SILPO	Q5lms6 silicibacte	947	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
875	57	12.4	461	2	Q5LMS6_SILPO	Q5lms6 silicibacte	948	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
876	57	12.4	468	2	Q5LMS6_SILPO	Q5lms6 silicibacte	949	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
877	57	12.4	471	2	Q5LMS6_SILPO	Q5lms6 silicibacte	950	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
878	57	12.4	477	2	Q5LMS6_SILPO	Q5lms6 silicibacte	951	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
879	57	12.4	477	2	Q5LMS6_SILPO	Q5lms6 silicibacte	952	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
880	57	12.4	477	2	Q5LMS6_SILPO	Q5lms6 silicibacte	953	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
881	57	12.4	477	2	Q5LMS6_SILPO	Q5lms6 silicibacte	954	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
882	57	12.4	477	2	Q5LMS6_SILPO	Q5lms6 silicibacte	955	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
883	57	12.4	477	2	Q5LMS6_SILPO	Q5lms6 silicibacte	956	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
884	57	12.4	477	2	Q5LMS6_SILPO	Q5lms6 silicibacte	957	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
885	57	12.4	478	2	Q5LMS6_SILPO	Q5lms6 silicibacte	958	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
886	57	12.4	478	2	Q5LMS6_SILPO	Q5lms6 silicibacte	959	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
887	57	12.4	487	1	P5BC_P0RPU	Q5lms6 silicibacte	960	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
888	57	12.4	487	1	P5BC_P0RPU	Q5lms6 silicibacte	961	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
889	57	12.4	487	2	Q5LMS6_SILPO	Q5lms6 silicibacte	962	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
890	57	12.4	493	2	Q5LMS6_SILPO	Q5lms6 silicibacte	963	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
891	57	12.4	494	1	ILVC_PHOPR	Q5lms6 silicibacte	964	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
892	57	12.4	517	2	Q5LMS6_SILPO	Q5lms6 silicibacte	965	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
893	57	12.4	531	2	Q5LMS6_SILPO	Q5lms6 silicibacte	966	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
894	57	12.4	534	2	Q5LMS6_SILPO	Q5lms6 silicibacte	967	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
895	57	12.4	535	2	Q5LMS6_SILPO	Q5lms6 silicibacte	968	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
896	57	12.4	576	2	Q5LMS6_SILPO	Q5lms6 silicibacte	969	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
897	57	12.4	606	2	Q5LMS6_SILPO	Q5lms6 silicibacte	970	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
898	57	12.4	610	2	Q5LMS6_SILPO	Q5lms6 silicibacte	971	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
899	57	12.4	610	2	Q5LMS6_SILPO	Q5lms6 silicibacte	972	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
900	57	12.4	629	2	Q5LMS6_SILPO	Q5lms6 silicibacte	973	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
901	57	12.4	633	2	Q5LMS6_SILPO	Q5lms6 silicibacte	974	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
902	57	12.4	641	2	Q5LMS6_SILPO	Q5lms6 silicibacte	975	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
903	57	12.4	689	2	Q5LMS6_SILPO	Q5lms6 silicibacte	976	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
904	57	12.4	695	2	Q5LMS6_SILPO	Q5lms6 silicibacte	977	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
905	57	12.4	709	2	Q5LMS6_SILPO	Q5lms6 silicibacte	978	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
906	57	12.4	792	2	Q5LMS6_SILPO	Q5lms6 silicibacte	979	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte
907	57	12.4	802	2	Q5LMS6_SILPO	Q5lms6 silicibacte	980	57	12.4	3338	2	Q5LMS6_SILPO	Q5lms6 silicibacte

981	Q88LL0_PSEPK	387	2	Q88LL0_PSEPK	1054	56.5	12.3	758	2	Q811T2_RAT	Q811t2 rattus norv
982	Q6MLC9_BDEBA	391	2	Q6MLC9_BDEBA	1055	56.5	12.3	759	2	Q8HXV1_RABIT	Q8hxl1 corytolagus
983	Q81JG4_BACAN	393	2	Q81JG4_BACAN	1056	56.5	12.3	769	2	Q811T3_RAT	Q811t3 rattus norv
984	Q7QAA4_ANOGA	394	2	Q7QAA4_ANOGA	1057	56.5	12.3	783	2	Q5NXT1_AZOSE	Q5nxt1 azoarcus sp
985	Q8LRB6_ORYSA	398	2	Q8LRB6_ORYSA	1058	56.5	12.3	852	1	YKML1_YEAST	P32330 saccharomyc
986	Q7WOP4_BORPE	403	2	Q7WOP4_BORPE	1059	56.5	12.3	856	2	Q6G429_BAHE	Q6g429 bartonella
987	Q7W3G0_BORPE	403	2	Q7W3G0_BORPE	1060	56.5	12.3	889	1	KCNC3_RAT	Q01956 rattus norv
988	Q7WET0_BORPE	403	2	Q7WET0_BORPE	1061	56.5	12.3	894	2	Q5CGN7_CRYHO	Q5cgn7 corytopospori
989	Q4J3V8_AZOV1	407	2	Q4J3V8_AZOV1	1062	56.5	12.3	933	2	Q83GL1_TROWH	Q83gl1 tropheryma
990	Q8E1S5_SHEON	408	2	Q8E1S5_SHEON	1063	56.5	12.3	939	2	Q83HL6_TROWH	Q83hl6 tropheryma
991	Q6LM16_PHOPR	409	2	Q6LM16_PHOPR	1064	56.5	12.3	1000	2	Q5U635_HUMAN	Q5u635 homo sapien
992	Q7P149_CHRVO	411	2	Q7P149_CHRVO	1065	56.5	12.3	1009	2	Q5Q208_IDILO	Q5q208 idiomarina
993	Q4SS40_TETNG	414	2	Q4SS40_TETNG	1066	56.5	12.3	1030	1	SEM6A_HUMAN	Q5h266 homo sapien
994	Q96JU9_HUMAN	418	2	Q96JU9_HUMAN	1067	56.5	12.3	1058	2	Q5P5T6_AZOSE	Q5p5t6 azoarcus sp
995	Q96JU9_HUMAN	418	2	Q96JU9_HUMAN	1068	56.5	12.3	1127	2	Q4YV05_PLABE	Q4yv05 plasmodium
996	CARP_CRYPA	419	1	CARP_CRYPA	1069	56.5	12.3	1241	2	Q60RT2_CABER	Q60rt2 caenorhabdi
997	Q5P850_ANAMM	422	2	Q5P850_ANAMM	1070	56.5	12.3	1250	2	Q4PLV2_USTMA	Q4plv2 ustilago ma
998	Q59H29_HUMAN	428	2	Q59H29_HUMAN	1071	56.5	12.3	1250	2	Q5ZCR4_ORYSA	Q5zcr4 oryza sativ
999	Q5QX17_IDILO	442	2	Q5QX17_IDILO	1072	56.5	12.3	1250	2	Q4SXM5_TETNG	Q4sxm5 tetraodon n
1000	NORM_SYNPF	464	1	NORM_SYNPF	1073	56.5	12.3	1739	2	Q414N8_GIBZE	Q414n8 gibberella
1001	Q63PW6_BURPS	468	2	Q63PW6_BURPS	1074	56.5	12.3	1778	2	Q6BCJ9_TETTH	Q6bcj9 tetrahymena
1002	Q2G6G2_BURMA	468	2	Q2G6G2_BURMA	1075	56.5	12.3	1838	2	Q5BDW2_EMENI	Q5bdw2 aspergillus
1003	Q49635_ARATH	471	2	Q49635_ARATH	1076	56.5	12.3	1844	2	Q4RMA1_TETNG	Q4rma1 tetraodon n
1004	Q5SWA9_CRYNE	474	2	Q5SWA9_CRYNE	1077	56.5	12.3	2113	2	Q6FNY7_CANGA	Q6fny7 candida gla
1005	Q8SDN4_9CAUD	484	2	Q8SDN4_9CAUD	1078	56.5	12.3	2217	2	Q4QB73_LEIMA	Q4qb73 leishmania
1006	Q4ZCK1_9VIRU	484	2	Q4ZCK1_9VIRU	1079	56.5	12.3	2876	2	Q7RL36_PLAYO	Q7rl36 plasmodium
1007	Q6GGS4_STAAC	484	2	Q6GGS4_STAAC	1080	56.5	12.3	4464	2	Q8E590_STRA3	Q8e590 streptococc
1008	Q5H1X6_STAAC	484	2	Q5H1X6_STAAC	1081	56.5	12.3	75	2	Q8E590_STRA3	Q8e590 streptococc
1009	Q7CZT7_AGR75	485	2	Q7CZT7_AGR75	1082	56.5	12.3	79	1	IVBK1_DENPO	P00981 dendroaspis
1010	Q90YV3_XENULA	485	2	Q90YV3_XENULA	1083	56.5	12.3	100	2	Q6N981_RHOPA	Q6n981 rhodopsuendo
1011	Q4PCU5_USTMA	491	2	Q4PCU5_USTMA	1084	56.5	12.3	103	1	NIRC_PARDE	Q51702 paracoccus
1012	Q86S12_9DIPT	494	2	Q86S12_9DIPT	1085	56.5	12.3	126	2	Q57316_9BACT	Q57316 mus musculu
1013	Q9RF10_MYXXA	500	2	Q9RF10_MYXXA	1086	56.5	12.3	126	2	Q57316_9BACT	Q57316 mus musculu
1014	ZGPAT1_MOUSE	511	1	ZGPAT1_MOUSE	1087	56.5	12.3	126	2	Q4JUN4_ECOLI	Q4jun4 escherichia
1015	Q7RYH0_NEUCR	521	2	Q7RYH0_NEUCR	1088	56.5	12.3	146	2	Q4NYQ0_9DELT	Q4nyq0 anaeromyxob
1016	Q567M8_BRARE	523	2	Q567M8_BRARE	1089	56.5	12.3	160	2	Q61TQ7_CABER	Q61tq7 caenorhabdi
1017	TH2A_TRYBB	529	1	TH2A_TRYBB	1090	56.5	12.3	177	2	Q62579_GIALA	Q62579 giardia lam
1018	Q4JXL7_CORJK	539	1	Q4JXL7_CORJK	1091	56.5	12.3	196	1	Y2B6_MYCCE	Q7r002 giardia lam
1019	Q4K108_PSEF5	557	2	Q4K108_PSEF5	1092	56.5	12.3	197	2	Q5F0H6_GLOX	P47528 mycoplasma
1020	Q4WD85_ASPFU	561	2	Q4WD85_ASPFU	1093	56.5	12.3	212	2	Q87MV9_VIBPA	Q5fuh6 gluconobact
1021	Q850S0_OINSE	570	2	Q850S0_OINSE	1094	56.5	12.3	212	2	Q87MV9_VIBPA	Q5fuh6 gluconobact
1022	S13A1_HUMAN	572	1	S13A1_HUMAN	1095	56.5	12.3	218	2	Q87MV9_VIBPA	Q5fuh6 gluconobact
1023	Q9BAR2_9MAGN	595	1	Q9BAR2_9MAGN	1096	56.5	12.3	220	2	Q5LEB4_BACFN	Q5leeb4 bacteroides
1024	Q31615_BACSU	608	2	Q31615_BACSU	1097	56.5	12.3	222	2	Q9KVFS_VIBCH	Q9kvfs vibrio chol
1025	Q69290_MOUSE	614	2	Q69290_MOUSE	1098	56.5	12.3	228	2	Q5J432_SALCH	Q5j432 salmonella
1026	Q5F0H5_GLOUX	624	2	Q5F0H5_GLOUX	1099	56.5	12.3	230	2	Q5QLP9_ORYSA	Q5qlp9 oryza sativ
1027	Q32212_BACSU	648	2	Q32212_BACSU	1100	56.5	12.3	242	2	Q6MEA9_PARUM	Q6mea9 parachlamyd
1028	Q9BAQ3_9MAGN	670	2	Q9BAQ3_9MAGN	1101	56.5	12.3	249	2	Q5VTN6_BRARE	Q5vtn6 brachydanio
1029	Q5CV27_CRYPV	681	2	Q5CV27_CRYPV	1102	56.5	12.3	254	2	Q91207_ONCMY	Q91207 oncorhynch
1030	Q9BAS3_9MAGN	683	2	Q9BAS3_9MAGN	1103	56.5	12.3	261	2	Q8UAP2_AGR75	Q8uap2 agrobacteri
1031	VGLH_PRYKA	686	1	VGLH_PRYKA	1104	56.5	12.3	264	2	Q9CFG1_PASMU	Q9cpg1 pasteurella
1032	VGLH_PRYN3	686	1	VGLH_PRYN3	1105	56.5	12.3	274	2	Q4NIS8_9MICC	Q4nis8 arthrobacte
1033	VGLH_PRYV1	686	1	VGLH_PRYV1	1106	56.5	12.3	279	1	Y170_BUCBP	Q89a82 buchnera ap
1034	Q5PPA2_9ALPH	686	1	Q5PPA2_9ALPH	1107	56.5	12.3	281	2	Q7NU04_CHRVO	Q7nu04 chromobacte
1035	Q9BAS8_9MAGN	688	2	Q9BAS8_9MAGN	1108	56.5	12.3	282	2	Q5FIQ7_LACAC	Q5fiq7 lactobacill
1036	Q7Q3N1_ANOGA	689	2	Q7Q3N1_ANOGA	1109	56.5	12.3	283	2	Q525Q1_MAGGR	Q525q1 magnaporthe
1037	Q9BAS2_9MAGN	690	2	Q9BAS2_9MAGN	1110	56.5	12.3	286	2	Q9CMZ4_PASMU	Q9cmz4 pasteurella
1038	Q9BAS4_9MAGN	690	2	Q9BAS4_9MAGN	1111	56.5	12.3	292	2	Q9U8W8_TACTR	Q9u8w8 tachypleus
1039	Q9BAQ8_EUXSE	691	2	Q9BAQ8_EUXSE	1112	56.5	12.3	294	2	Q6FFJ6_ACIAD	Q6ffj6 acinetobact
1040	Q9BAQ9_9MAGN	692	2	Q9BAQ9_9MAGN	1113	56.5	12.3	295	2	Q7NFB8_GLOVI	Q7nfb8 gloeobacter
1041	Q9BAR0_9MAGN	692	2	Q9BAR0_9MAGN	1114	56.5	12.3	302	2	Q7Q9G8_ANOGA	Q7q9g8 anopheles g
1042	Q9BAS5_9MAGN	692	2	Q9BAS5_9MAGN	1115	56.5	12.3	304	2	Q8ESB3_OCEIH	Q8esb3 oceanobacil
1043	Q9BAS5_9MAGN	692	2	Q9BAS5_9MAGN	1116	56.5	12.3	306	2	Q87HY7_VIBPA	Q87hy7 vibrio para
1044	Q9BAS7_9MAGN	695	2	Q9BAS7_9MAGN	1117	56.5	12.3	319	2	Q611Y3_CABER	Q611y3 caenorhabdi
1045	Q96SW4_HUMAN	699	2	Q96SW4_HUMAN	1118	56.5	12.3	324	2	Q5O5K1_MOUSE	Q5o5k1 mus musculu
1046	Q9SC14_EUXSE	704	2	Q9SC14_EUXSE	1119	56.5	12.3	325	2	Q5F487_FISMU	Q5f487 fischerella
1047	Q9BAS6_9MAGN	707	2	Q9BAS6_9MAGN	1120	56.5	12.3	334	2	Q36172_9VIRU	Q36172 rice grassy
1048	Q6C6N0_YARLI	710	2	Q6C6N0_YARLI	1121	56.5	12.3	340	2	Q52W82_9RHOD	Q52w82 compopogon
1049	Q8HTM7_PODPE	726	2	Q8HTM7_PODPE	1122	56.5	12.3	342	2	Q5O4U7_HUMAN	Q5o4u7 homo sapien
1050	Q8HTM9_9MAGN	726	2	Q8HTM9_9MAGN	1123	56.5	12.3	344	2	Q8F9S3_LEPIN	Q8f9s3 leptospira
1051	Q5PKX6_RAT	739	2	Q5PKX6_RAT	1124	56.5	12.3	344	2	Q5B7Z1_EMENI	Q5b7z1 aspergillus
1052	Q5PKX5_RAT	730	2	Q5PKX5_RAT	1125	56.5	12.3	344	2	Q5AAH7_EMENI	Q5aah7 aspergillus
1053	Q5PKX5_RAT	730	2	Q5PKX5_RAT	1126	56.5	12.3	352	2	Q8E5M8_RHIL0	Q8e5m8 rhizobium l
										Q6YT41_PIG	Q6yt41 sus scrofa

1127	56	12.1	354	2	Q6F593 ANAPL	Q6f593 anas platyr	1200	56	12.1	568	2	Q4FXC6 LEIMA	Q4fxc6 leishmania
1128	56	12.1	359	2	Q5Z1V1 NOCPA	Q5z1v1 nocardia fa	1201	56	12.1	575	2	Q7N243 PHOHL	Q7n243 photorhabdu
1129	56	12.1	361	2	Q6Z896 ICTPU	Q6z896 ictalurus p	1202	56	12.1	576	2	Q7N7S6 PHOHL	Q7n7s6 photorhabdu
1130	56	12.1	363	2	Q8BNF7 PSEPK	Q8bnf7 pseudomonas	1203	56	12.1	578	1	PTF3E RHOC	Ptf3e r pts svate
1131	56	12.1	364	2	Q5UZ44 HALMA	Q5uz44 haloarcula	1204	56	12.1	581	2	Q8C3F7 MOUSE	Q8c3f7 mus musculus
1132	56	12.1	365	2	Q98IE3 RHIZO	Q98ie3 rhizobium 1	1205	56	12.1	594	2	Q9X3S5 PSEAE	Q9x3s5 pseudomonas
1133	56	12.1	376	2	Q6CNV1 KLULA	Q6cnv1 kluyveromyc	1206	56	12.1	605	2	Q6INM3 XENLA	Q6inm3 xenopus lae
1134	56	12.1	388	2	Q8STX2 ARATH	Q8stx2 arabidopeis	1207	56	12.1	610	2	Q76486 LEIME	Q76486 leishmania
1135	56	12.1	388	2	Q673W2 MOUSE	Q673w2 mus musculu	1208	56	12.1	621	2	Q4PHM9 USTWA	Q4phm9 ustilago ma
1136	56	12.1	398	2	Q7XKE3 ORISA	Q7xke3 oryza sativ	1209	56	12.1	621	2	Q660P2 BORG	Q660p2 borrelia ga
1137	56	12.1	405	2	Q7NYU3 CHRYO	Q7nyu3 chromobacte	1210	56	12.1	626	2	Q51574 BORG	Q51574 borrelia bu
1138	56	12.1	408	2	Q7PW26 ANOHA	Q7pw26 anopheles g	1211	56	12.1	632	2	Q4SUG4 TETNG	Q4sug4 tetraodon n
1139	56	12.1	409	2	Q87LW6 VIBPA	Q87lw6 vibrio para	1212	56	12.1	639	2	Q93MA1 CLOPE	Q93ma1 clostridm n
1140	56	12.1	411	2	Q9A4V3 CAUCR	Q9a4v3 caulobacter	1213	56	12.1	638	2	Q8C4I5 MOUSE	Q8c4i5 mus musculu
1141	56	12.1	413	2	Q67T35 SYMTH	Q67t35 symbiobacte	1214	56	12.1	643	2	Q5QNS3 ORYSA	Q5qns3 oryza sativ
1142	56	12.1	434	1	ENO DESVM	Q32513 desulfovibr	1215	56	12.1	653	1	KCNAA HUMAN	P22459 homo sapien
1143	56	12.1	436	1	ALBD1 BACSU	P71008 bacillus su	1216	56	12.1	690	2	Q73T97 MYCPA	Q73t97 mycobacteri
1144	56	12.1	436	1	ALBD2 BACSU	Q8rkH4 bacillus su	1217	56	12.1	712	2	Q54QS3 DICDI	Q54qs3 dictyosteli
1145	56	12.1	438	2	Q9KYG4 STRCO	Q9kyg4 streptomyce	1218	56	12.1	724	2	Q8ABY9 BACTN	Q8aby9 bacteroides
1146	56	12.1	439	2	Q6BRK2 DEBHA	Q6brk2 debaryomyce	1219	56	12.1	736	2	Q28661 ARCFU	Q28661 archaeoglob
1147	56	12.1	440	2	Q8UI28 AGRT5	Q8ui28 agrobacteri	1220	56	12.1	752	2	Q4NY34 9DELT	Q4ny34 anaeromyxob
1148	56	12.1	442	2	Q642S2 XENLA	Q642s2 xenopus lae	1221	56	12.1	848	2	Q5EES4 RHIME	Q5ees4 human immun
1149	56	12.1	445	2	Q4HBN0 9DEIO	Q4hbn0 deinococcus	1222	56	12.1	855	2	Q8A6V6 BACTN	Q8a6v6 bacteroides
1150	56	12.1	449	2	Q06407 MYCTO	Q06407 mycobacteri	1223	56	12.1	917	2	Q4WEX4 ASPFU	Q4wex4 aspergillus
1151	56	12.1	449	2	Q7UI76 MYCBO	Q7uit6 mycobacteri	1224	56	12.1	965	2	Q5OLF0 SCORY	Q5olf0 corynebacte
1152	56	12.1	450	2	Q6A675 PROAC	Q6a6t5 propionibac	1225	56	12.1	1012	2	Q7RCQ7 PLAYO	Q7rcq7 plasmodium
1153	56	12.1	452	2	Q6D0K7 ERWCT	Q6d0k7 erwinnia car	1226	56	12.1	1051	2	Q5ZD75 ORYSA	Q5zd75 oryza sativ
1154	56	12.1	456	2	Q84DN6 LISMO	Q84dm6 listeria mo	1227	56	12.1	1084	2	Q5VWH5 LEGPL	Q5vwh5 legionella
1155	56	12.1	456	2	Q84DN8 LISMO	Q84dm8 listeria mo	1228	56	12.1	1118	2	Q68M96 RHIME	Q68m96 rhizobium m
1156	56	12.1	456	2	Q84DN9 LISMO	Q84dm9 listeria mo	1229	56	12.1	1118	2	Q92Y97 RHIME	Q92y97 rhizobium m
1157	56	12.1	457	1	DCR1B CHICK	Q5qjc3 gallus gall	1230	56	12.1	1126	2	Q4PEF6 USTWA	Q4pef6 ustilago ma
1158	56	12.1	457	2	Q84DN7 LISMO	Q84dm7 listeria mo	1231	56	12.1	1135	2	Q5X437 LEGPA	Q5x437 legionella
1159	56	12.1	457	2	Q84DN4 LISMO	Q84dp4 listeria mo	1232	56	12.1	1243	2	Q4FRM6 9GAMM	Q4frm6 psychrobact
1160	56	12.1	458	2	Q84DN5 LISMO	Q84dn5 listeria mo	1233	56	12.1	1305	1	FTSK YERPE	Q8zgc7 versinia pe
1161	56	12.1	458	2	Q84DN6 LISMO	Q84dn6 listeria mo	1234	56	12.1	1310	2	Q66CK2 YERPS	Q66ck2 versinia ps
1162	56	12.1	459	2	Q5FWL2 XENLA	Q5fwl2 xenopus lae	1235	56	12.1	1384	1	CNTPL HUMAN	P83357 homo sapien
1163	56	12.1	461	2	Q84D05 LISMO	Q84dq5 listeria mo	1236	56	12.1	1406	2	Q6L3G4 SOLDE	Q6l3g4 solanum dem
1164	56	12.1	461	2	Q82D13 BURMA	Q82dl3 burkholderi	1237	56	12.1	1439	2	Q7XQP1 ORYSA	Q7xqp1 oryza sativ
1165	56	12.1	471	2	Q84DQ3 LISMO	Q84dq3 listeria mo	1238	56	12.1	1462	2	Q8I1W9 PLAF7	Q8i1w9 plasmodium
1166	56	12.1	477	2	Q84DN5 LISMO	Q84dn5 listeria mo	1239	56	12.1	1520	2	Q5SUF6 CRYNE	Q5suf6 cryptococcu
1167	56	12.1	477	2	Q84DN0 LISMO	Q84dn0 listeria mo	1240	56	12.1	1608	2	Q59GL0 HUMAN	Q59gl0 homo sapien
1168	56	12.1	477	2	Q84DN1 LISMO	Q84dn1 listeria mo	1241	56	12.1	1856	1	GBF1 CRIGR	Q9fid7 cricetus
1169	56	12.1	478	2	Q84DN3 LISMO	Q84dn3 listeria mo	1242	56	12.1	1859	1	GBF1 HUMAN	Q92c28 homo sapien
1170	56	12.1	478	2	Q84DP0 LISMO	Q84dp0 listeria mo	1243	56	12.1	1875	2	Q6RCQ2 LEGPN	Q6rcq2 legionella
1171	56	12.1	479	2	Q84DP3 LISMO	Q84dp3 listeria mo	1244	56	12.1	1875	2	Q5Z276 LEGPH	Q5z276 legionella
1172	56	12.1	480	2	Q4NEK3 9MICC	Q4nek3 arthrobacte	1245	56	12.1	1914	1	RLF HUMAN	Q13129 homo sapien
1173	56	12.1	490	2	Q7N3C6 PHOLL	Q7n3c6 photorhabdu	1246	56	12.1	1914	2	Q5RCL4 PONPY	Q5rcl4 pongo pygma
1174	56	12.1	494	2	Q5V4M5 HALMA	Q5v4m5 haloarcula	1247	56	12.1	1914	2	Q8VXB6 MUSCULU	Q8vxb6 mus musculu
1175	56	12.1	503	1	VUL HPV32	P36737 human papil	1248	56	12.1	2055	1	MPDZ MOUSE	Q8vxb6 mus musculu
1176	56	12.1	503	2	Q5N550 SYNPE	Q5n550 synchococc	1249	56	12.1	3972	2	Q7PMJ6 ANOHA	Q7pmj6 anopheles g
1177	56	12.1	508	2	Q8FP11 COREF	Q8fp11 corynebacte	1250	56	12.1	6994	2	Q17343 CAESL	Q17343 caenorhabdi
1178	56	12.1	516	2	Q8CE47 MOUSE	Q8ce47 mus musculu	1251	56	12.0	62	2	Q8CTK3 YERPE	Q8ctk3 versinia pe
1179	56	12.1	516	2	Q94WJ7 CTEFR	Q94wj7 ctenogobio	1252	56	12.0	63	2	Q8CTK3 YERPE	Q8ctk3 versinia pe
1180	56	12.1	518	2	Q4IHP5 GIBZE	Q4ihp5 gibberella	1253	56	12.0	84	2	Q8LJ31 PSEPK	Q8lj31 pseudomonas
1181	56	12.1	518	2	Q4IHP5 GIBZE	Q4ihp5 gibberella	1254	56	12.0	124	2	Q6TSR7 BACCE	Q6tsr7 bacillus ce
1182	56	12.1	519	2	Q3VXK1 DROME	Q3vxx1 drosophila	1255	56	12.0	134	2	Q5TLI8 MOUSE	Q5tli8 mus musculu
1183	56	12.1	524	2	Q8IF66 BACCR	Q8ife6 bacillus ce	1256	56	12.0	138	2	Q6YXP7 PHIPA	Q6yxp7 physcomitre
1184	56	12.1	525	2	Q4RW80 TETNG	Q4rw80 tetraodon n	1257	56	12.0	141	2	Q63K49 BURPS	Q63k49 burkholderi
1185	56	12.1	528	2	Q4KCT5 PSEF5	Q4kct5 pseudomonas	1258	56	12.0	147	2	Q62B21 BURMA	Q62b21 burkholderi
1186	56	12.1	531	2	Q4I973 GIBZE	Q4i973 gibberella	1259	56	12.0	147	2	Q62B21 BURMA	Q62b21 burkholderi
1187	56	12.1	539	1	CH60 ENTAS	Q62200 enterobacte	1260	56	12.0	151	2	Q93Z87 BROIN	Q93z87 bromus iner
1188	56	12.1	539	1	CH60 ENTAS	Q62190 enterobacte	1261	56	12.0	157	2	Q6U398 LACPL	Q6u398 lactobacill
1189	56	12.1	540	1	CH60 KLEOX	Q62210 klebsiella	1262	56	12.0	168	2	Q4IXV9 BURK	Q4ixv9 burkholderi
1190	56	12.1	540	1	CH60 KLEOX	Q62210 klebsiella	1263	56	12.0	177	2	Q6LME1 PHOPR	Q6lme1 photobacter
1191	56	12.1	544	1	CH60 AERSA	Q68309 aeromonas s	1264	56	12.0	179	2	Q7BKFS PRB01	Q7bkfs gamma-prote
1192	56	12.1	545	2	Q6TLJ7 9PSED	Q6tlj7 pseudomonas	1265	56	12.0	184	2	Q83JMS SHIGEL	Q83jms shigella fi
1193	56	12.1	547	1	CH60 KLEPN	Q66026 klebsiella	1266	56	12.0	186	2	Q5M7K0 XENTR	Q5m7k0 xenopus tro
1194	56	12.1	547	2	Q92Z88 RHIME	Q92z88 rhizobium m	1267	56	12.0	186	2	Q707B6 ECOLI	Q707b6 escherichia
1195	56	12.1	548	2	Q8Y3X3 XENNE	Q8y3x3 xenorhabdus	1268	56	12.0	187	2	Q8CVQ9 ECOL6	Q8cvq9 escherichia
1196	56	12.1	557	1	FN04 HUMAN	P31512 homo sapien	1269	56	12.0	187	2	Q8E5S2 FUGRU	Q8e5s2 fugu rubrip
1197	56	12.1	557	1	Q5RDN6 PONPY	Q5rdn6 pongo pygma	1270	56	12.0	191	2	Q6E5S2 FUGRU	Q6e5s2 fugu rubrip
1198	56	12.1	558	2	Q53XR0 HUMAN	Q53xr0 homo sapien	1271	56	12.0	194	1	CLMP22 HUMAN	Q9y584 homo sapien
1199	56	12.1	559	2	Q6UN75 TOBAC	Q6un75 nicotiana t	1272	56	12.0	196	1	CLPP1_PROMP	Q7v1w0 prochloroco



1273	55.5	12.0	198	2	Q87A07_XYLEFT	Q87A07_xylella fas	1346	55.5	12.0	382	2	Q5BIP0_BOVIN	Q5BIP0_bos taurus
1274	55.5	12.0	199	2	Q65D47_BACLD	Q65d47 bacillus li	1347	55.5	12.0	383	1	YJK8_YEAST	P42946_saccharomyc
1275	55.5	12.0	206	2	Q5SE77_BRAOL	Q5se77 brassica ol	1348	55.5	12.0	383	2	Q6QSN7_YEAST	Q6qsn7_saccharomyc
1276	55.5	12.0	211	2	Q9NA02_9CRUS	Q9na02 daphnia mag	1349	55.5	12.0	383	2	Q5ZOK5_NOCFA	Q5zok5_nocardia fa
1277	55.5	12.0	213	2	Q9NA09_CABEL	Q9na09 caenorhabdi	1350	55.5	12.0	384	2	Q9L138_BRANA	Q9l138_brassica na
1278	55.5	12.0	214	2	Q61ZM4_CABEL	Q61zm4 caenorhabdi	1351	55.5	12.0	384	2	Q9LIA9_ARATH	Q9lia9_arabidopsis
1279	55.5	12.0	221	2	Q6CL37_KLULA	Q6cl37 kluyveromyc	1352	55.5	12.0	385	2	Q9FX15_ARATH	Q9fx15_arabidopsis
1280	55.5	12.0	223	2	Q9DC94_MOUSE	Q9dc94 mus musculu	1353	55.5	12.0	389	2	Q6PQ18_DIGPU	Q6pq18_digitalis p
1281	55.5	12.0	232	2	Q8B5R5_9TOMB	Q8b5r5 beet black	1354	55.5	12.0	389	2	Q5HV30_CAMUR	Q5hv30_campylobact
1282	55.5	12.0	235	2	Q4IQA6_9HURK	Q4iqae burkholderi	1355	55.5	12.0	389	2	Q9PPF7_CAMUJ	Q9ppf7_campylobact
1283	55.5	12.0	237	2	Q4I9H8_GIBZE	Q4i9h8 gibberella	1356	55.5	12.0	393	2	Q4NU11_9DELT	Q4nu11_aeaeoromycob
1284	55.5	12.0	237	2	Q4ZQ49_PSESY	Q4zq49 pseudomonas	1357	55.5	12.0	394	2	Q560G3_CRYNE	Q560g3_cryptococcu
1285	55.5	12.0	237	2	Q8B5Y3_PSESM	Q8b5y3 pseudomonas	1358	55.5	12.0	407	2	Q947C6_TRIMO	Q947c6_triticum mo
1286	55.5	12.0	240	2	Q8XW05_RALSO	Q8xw05 ralsstonia s	1359	55.5	12.0	409	2	Q4NRD2_9DELT	Q4nrd2_aeaeoromycob
1287	55.5	12.0	245	2	Q98R89_WYCPU	Q98r89 mycoplasma	1360	55.5	12.0	414	2	Q7MHX0_VIBVY	Q7mhx0_vibrio vuln
1288	55.5	12.0	245	2	Q7ZYWI_BRARE	Q7zywi brachydanio	1361	55.5	12.0	417	2	Q9ZIS3_ECOLI	Q9zis3_escherichia
1289	55.5	12.0	248	2	Q6CA49_YARLI	Q6ca49 yarrowia li	1362	55.5	12.0	425	2	Q5WRV3_LEGPL	Q5wrv3_legionella
1290	55.5	12.0	250	2	Q89L47_BRAJA	Q89l47 bradyrhizob	1363	55.5	12.0	425	2	Q5WXT6_LEGPL	Q5wxt6_legionella
1291	55.5	12.0	253	2	Q7PJ20_ANOGA	Q7pj20 anopheles g	1364	55.5	12.0	425	2	Q5XG66_LEGPA	Q5xg66_legionella
1292	55.5	12.0	253	2	Q8FP86_COREF	Q8fp86 corynebacte	1365	55.5	12.0	431	2	Q9MS90_9MAGN	Q9ms90_austrobaile
1293	55.5	12.0	254	2	Q9RWPI_DEIRA	Q9rwpl deinococcus	1366	55.5	12.0	437	2	Q83CE5_CORBU	Q83ce5_coxiella bu
1294	55.5	12.0	256	2	Q9RUK4_DEIRA	Q9ruk4 deinococcus	1367	55.5	12.0	451	2	Q4NWM3_9DELT	Q4nwm3_aeaeoromycob
1295	55.5	12.0	257	1	PEBB_PROMM	Q7v585 prochloroc	1368	55.5	12.0	452	2	Q8KAS7_CHEITE	Q8kas7_chlorobium
1296	55.5	12.0	262	1	BACR_HALSA	P02945 halobacteri	1369	55.5	12.0	456	2	Q20523_CABEL	Q20523_caenorhabdi
1297	55.5	12.0	262	2	Q5HL72_STAEO	Q5hl72 staphylococ	1370	55.5	12.0	459	2	Q9CIK1_LACLA	Q9c1k1_lactococcus
1298	55.5	12.0	262	2	Q4G5W6_BRARE	Q4g5w6 brachydanio	1371	55.5	12.0	470	2	Q7MSR1_WOLSU	Q7msr1_wolinella s
1299	55.5	12.0	263	2	Q5CVI7_CRYPV	Q5cvy7 cryptospori	1372	55.5	12.0	471	2	Q5FT20_GLUOX	Q5ft20_gluconobact
1300	55.5	12.0	263	2	Q5CFK0_CRYHO	Q5cfk0 cryptospori	1373	55.5	12.0	483	2	Q9I829_ONCMY	Q9i829_oncorhynch
1301	55.5	12.0	270	2	Q5VU30_HUMAN	Q5vu30 homo sapien	1374	55.5	12.0	484	2	Q4ZCR7_9VIRU	Q4zcr7_bacterioph
1302	55.5	12.0	270	2	Q98866_BRARE	Q98866 brachydanio	1375	55.5	12.0	484	2	Q73RS3_TREDE	Q73rs3_treponema d
1303	55.5	12.0	283	2	Q5V2V1_HALMA	Q5v2v1 haloarcula	1376	55.5	12.0	484	2	Q8NWL7_STAAM	Q8nwl7_staphylococ
1304	55.5	12.0	292	2	Q91XR2_CAVPO	Q91xr2 cavia porce	1377	55.5	12.0	516	2	Q5JBE0_9LILI	Q5jbe0_toxicocord
1305	55.5	12.0	295	2	Q6GNN7_XENLA	Q6gnn7 xenopus lae	1378	55.5	12.0	522	2	Q8DSQ2_VIBVU	Q8dsq2_vibrio vuln
1306	55.5	12.0	299	2	Q9HZ18_PSEAE	Q9hz18 pseudomonas	1379	55.5	12.0	528	2	Q7MCQ9_VIBVU	Q7mcq9_vibrio vuln
1307	55.5	12.0	300	2	Q5P736_AZOSE	Q5p736 azoarcus sp	1380	55.5	12.0	528	2	Q73KN8_TREDE	Q73kn8_treponema d
1308	55.5	12.0	309	2	Q8DPP1_STRRG	Q8dpp1 streptococc	1381	55.5	12.0	528	2	Q4RJ06_TETNG	Q4rj06_tetrasodon n
1309	55.5	12.0	309	2	Q97QL2_STRPN	Q97ql2 streptococc	1382	55.5	12.0	529	2	Q5CP72_CRYHO	Q5cp72_cryptospori
1310	55.5	12.0	312	1	CATO_MOUSE	Q8bm88 mus musculu	1383	55.5	12.0	545	2	Q8YPL8_ANASP	Q8ypl8_anabaena sp
1311	55.5	12.0	312	2	Q4QQL3_MOUSE	Q4qql3 mus musculu	1384	55.5	12.0	545	2	Q9PXA4_9PARA	Q9pxa4_measles vir
1312	55.5	12.0	315	2	Q6LHU3_PHOPR	Q6lhu3 photobacter	1385	55.5	12.0	546	2	Q9IHA5_9PARA	Q9iha5_rinderpest
1313	55.5	12.0	316	2	Q9RUAB_DEIRA	Q9ruab deinococcus	1386	55.5	12.0	553	2	Q9I180_9PARA	Q9i180_measles vir
1314	55.5	12.0	317	1	EXOZ_RHIME	P26502 rhizobium m	1387	55.5	12.0	562	1	Y3471_BRAVA	Q89pk9_bradyrhizob
1315	55.5	12.0	323	2	Q888H6_PSESM	Q888h6 pseudomonas	1388	55.5	12.0	566	2	Q5H4R5_XANOR	Q5h4r5_xanthomonas
1316	55.5	12.0	324	2	Q9BF59_ATEFU	Q9bf59 ateles fusc	1389	55.5	12.0	572	2	Q5R773_PONPY	Q5r773_pongo pygma
1317	55.5	12.0	325	2	Q6LG58_PHOPR	Q6lg58 photobacter	1390	55.5	12.0	580	2	Q98DA6_RHILQ	Q98da6_rhizobium l
1318	55.5	12.0	326	2	Q97C58_THEVO	Q97c58 thermoplas	1391	55.5	12.0	587	2	Q9FK05_ARATH	Q9fk05_arabidopsis
1319	55.5	12.0	326	2	Q9BF48_PIG	Q9bf48 sus scrofa	1392	55.5	12.0	595	2	Q5R5H6_PONPY	Q5r5h6_pongo pygma
1320	55.5	12.0	326	2	Q9BF60_LEMCA	Q9bf60 lemur catta	1393	55.5	12.0	596	2	Q7NJ84_GLOVI	Q7nj84_gloeobacter
1321	55.5	12.0	326	2	Q9BF72_SORAR	Q9bf72 sorex atane	1394	55.5	12.0	607	2	Q9C9Y1_ARATH	Q9c9y1_arabidopsis
1322	55.5	12.0	326	2	Q9BF75_MYRTR	Q9bf75 myrmecophag	1395	55.5	12.0	625	1	KCNC4_FAT	Q63734_rattus norv
1323	55.5	12.0	326	2	Q9BF76_TAMTE	Q9bf76 tamandua te	1396	55.5	12.0	628	1	KCNC4_MOUSE	Q8r1c0_mus musculu
1324	55.5	12.0	326	2	Q9NQ77_AGOTA	Q9nq77 agouti tacz	1397	55.5	12.0	631	2	Q7VND5_HAEDU	Q7vnd5_haemophilus
1325	55.5	12.0	326	2	Q99NQ9_HYDHY	Q99nq9 hydrochoeru	1398	55.5	12.0	631	2	Q803A6_BRARE	Q803a6_brachydanio
1326	55.5	12.0	326	2	Q99NR0_9HYST	Q99nr0 cavia tachu	1399	55.5	12.0	634	2	Q806J0_DROME	Q806j0_drosophila
1327	55.5	12.0	326	2	Q99NR3_EREDO	Q99nr3 erechizon d	1400	55.5	12.0	635	1	KCNC4_HUMAN	Q03721_homo sapien
1328	55.5	12.0	326	2	Q99NR4_HYSBR	Q99nr4 hystrix bra	1401	55.5	12.0	643	1	YKD6_CABEL	Q03564_caenorhabdi
1329	55.5	12.0	326	2	Q99NR8_CASCN	Q99nr8 castor cana	1402	55.5	12.0	648	1	PRIA_RICPR	Q9zdl0_rickettsia
1330	55.5	12.0	331	2	Q59NG1_CANAL	Q59ng1 candida alb	1403	55.5	12.0	662	1	HEFA_HHV6	F52375_human herpe
1331	55.5	12.0	331	2	Q5KPG4_CRYNE	Q5kpg4 cryptococcu	1404	55.5	12.0	678	2	Q82E42_STRAW	Q82e42_streptomyce
1332	55.5	12.0	336	2	Q4H4M1_9DETO	Q4h4m1 deinococcus	1405	55.5	12.0	687	2	Q9BXR8_HUMAN	Q9bxr8_homo sapien
1333	55.5	12.0	341	2	Q4H4Z8_9DETO	Q4h4z8 deinococcus	1406	55.5	12.0	698	2	Q84Z10_ORYSA	Q84z10_oryza sativ
1334	55.5	12.0	343	2	Q98865_BRARE	Q98865 brachydanio	1407	55.5	12.0	716	1	P5CS_ORYSA	Q04226_o delta l-p
1335	55.5	12.0	344	2	Q8YQ35_ANASP	Q8yq35 anabaena sp	1408	55.5	12.0	716	2	Q6PW76_ORYSA	Q6pw76_oryza sativ
1336	55.5	12.0	346	2	Q59293_PYRHO	Q59293 pyrococcus	1409	55.5	12.0	716	2	Q60EM4_ORYSA	Q60em4_oryza sativ
1337	55.5	12.0	346	2	Q740N5_MYCPA	Q740n5 mycobacteri	1410	55.5	12.0	726	2	Q8HTM8_9MAGN	Q8htm8_diphylleia
1338	55.5	12.0	357	2	Q80LT8_NPVAB	Q80lt8 adoxophyes	1411	55.5	12.0	740	2	Q8DJL7_SYNEL	Q8djl7_synchococc
1339	55.5	12.0	358	2	Q67TC7_SYMTH	Q67tc7 symbiobacte	1412	55.5	12.0	742	2	Q6MNV6_DDBEA	Q6mnv6_bdellovibri
1340	55.5	12.0	376	1	Q656_NPVAC	P41705 autographa	1413	55.5	12.0	751	2	Q9AYM4_VIGUN	Q9aym4_vigna ungui
1341	55.5	12.0	378	2	Q8B9E5_NPVRO	Q8b9e5 rachiplusia	1414	55.5	12.0	788	2	Q6INE9_XENLA	Q6ine9_xenopus lae
1342	55.5	12.0	379	1	Q656_NPVCF	P41718 choristoneu	1415	55.5	12.0	806	1	PAZG6_HUMAN	Q60733_homo sapien
1343	55.5	12.0	379	2	Q882F2_PSESM	Q882f2 pseudomonas	1416	55.5	12.0	806	2	Q7W7V0_BORPA	Q7w7v0_bordetella
1344	55.5	12.0	379	2	Q77DF6_NPVCF	Q77df6 choristoneu	1417	55.5	12.0	806	2	Q7WL90_BORBR	Q7wl90_bordetella
1345	55.5	12.0	381	2	Q82B18_STRAW	Q82b18 streptomyce	1418	55.5	12.0	806	2	Q7MP30_VIBVU	Q7mp30_vibrio vuln

1492	55	11.9	268	1	EA30_VICFA	P21745 vicia faba
1493	55	11.9	268	2	Q43675_VICFA	Q43675 vicia faba
1494	55	11.9	270	2	Q94006_CANAL	Q94006 candida alb
1495	55	11.9	270	2	Q5A4M8_CANAL	Q5a4m8 candida alb
1496	55	11.9	270	2	Q8BY39_MOUSE	Q8by39 mus musculus
1497	55	11.9	273	2	Q73NN2_TREDE	Q73nn2 treponema d
1498	55	11.9	275	2	Q54KD4_DICDI	Q54kd4 dictyosteli
1499	55	11.9	277	2	Q9FYE3_ARATH	Q9fye3 arabidopsis
1500	55	11.9	282	2	Q9Y4U1_HUMAN	Q9y4u1 homo sapien
ALIGNMENTS						
RESULT 1						
Q6UWZ1_HUMAN						
ID	Q6UWZ1	HUMAN	PRELIMINARY;	PRT;	89 AA.	
AC	Q6UWZ1					
DT	05-JUL-2004	(TrEMBLrel. 27, Created)				
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)				
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)				
DE	ERV526.					
GN	Name=EXYD4; ORFNames=UNQ526;					
OS	Homo sapiens (Human)					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;					
OC	Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
NUCLEOTIDE SEQUENCE.						
RA	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;					
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,					
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,					
RA	Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,					
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,					
RA	Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,					
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,					
RA	Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,					
RA	Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,					
RA	Wood W.I., Godowski P.J., Gray A.M.;					
RT	"The secreted protein discovery initiative (SPDI), a large-scale					
RT	effort to identify novel human secreted and transmembrane proteins: a					
RT	bioinformatics assessment.";					
RL	Genome Res. 13:2265-2270(2003).					
DR	ENBL; AY358584; AAQ88947.1; -; mRNA.					
DR	HGNC; HGNC:4028; FXID4.					
DR	GO; GO:0016020; C:membrane; IEA.					
DR	GO; GO:0005216; F:ion channel activity; IEA.					
DR	GO; GO:0006811; P:ion transport; IEA.					
DR	InterPro; IPR000272; FYD.					
DR	Pfam; PF02038; ATP1G_PLM_MAT8; 1.					
DR	PROSITE; PS01310; FYXD; 1.					
SQ	SEQUENCE 89 AA; 9433 MW; C5934288182449B0 CRC64;					
Query Match						
Best Local Similarity 100.0%; Score 461; DB:2; Length 89;						
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	1	MERTVALLLLAGLTALEANDPFANKDDPFYDWNKLSGLICGGLLAIGIAVLGSK	60			
Db	1	MERTVALLLLAGLTALEANDPFANKDDPFYDWNKLSGLICGGLLAIGIAVLGSK	60			
Qy	61	CKYSSQKQHPVPEKAIPITPGSATTC	89			
Db	61	CKYSSQKQHPVPEKAIPITPGSATTC	89			
RESULT 2						
Q7Z4M5_HUMAN						
ID	Q7Z4M5	HUMAN	PRELIMINARY;	PRT;	89 AA.	
AC	Q7Z4M5					
DT	01-OCT-2003	(TrEMBLrel. 25, Created)				
DT	01-OCT-2003	(TrEMBLrel. 25, Last sequence update)				



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13-SEP-2005 (TREMELrel. 31, Last annotation update)
DE FXVD domain containing ion transport regulator 4.
GN Name=FXVD4; ORFNames=RP11-92P6.2-004;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN RECONSTRUCTION FROM ESTS, AND CONCEPTUAL TRANSLATION.
RX MEDLINE=20408885; PubMed=10950925; DOI=10.1006/geno.2000.6274;
RA Sweadner K.J., Rael E.;
RT "The FXVD gene family of small ion transport regulators or channels:
RT cDNA sequence, protein signature sequence, and expression.";
RL Genomics 68:41-56(2000).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the FXVD family.
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CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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CC EMBL; AI829935; -, NOT_ANNOTATED_CDS; mRNA.
CC Ensembl; ENSG00000150201; Homo sapiens.
CC HGNC; HGNC:4028; FXVD4.
CC InterPro; IPR000272; FXVD.
CC Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
CC PROSITE; PS01310; FXVD_1.
KW Ion transport; Ionic channel; Signal; Transmembrane; Transport.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 89 FXVD domain-containing ion transport
FT regulator 4.
FT TOPO_DOM 21 38 Extracellular (Potential).
FT TRANSMEM 39 59 Potential.
FT TOPO_DOM 60 89 Cytoplasmic (Potential).
SQ SEQUENCE 89 AA; 9373 MW; B595EF99A4949B4 CRC64;

Query Match 97.6%; Score 450; DB 1; Length 89;
Best Local Similarity 97.8%; Pred. No. 4.5e-40;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MERVTLALLLAGLTALEANDPFANKDDPPYDWKNLQSLGICGGLTAGIAAVLSGK 60
Db 1 MERVTLALLLAGLTALEANDPFANKDDPPYDWKNLQSLGICGGLTAGIAAVLSGK 60
QY 61 CKYKSSQKQHSVPPEKAIPITPGSATTC 89
Db 61 CKKSSQKQHSVPPEKAIPITPGSATTC 89

RESULT 3
ID FXVD4_HUMAN STANDARD; PRT; 89 AA.
AC P59646;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE FXVD domain-containing ion transport regulator 4 precursor.

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```
RESULT 4
FYXD4 MOUSE
ID   FXD4_MOUSE STANDARD; PRT; 88 AA.
AC   Q9D2W0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   FXD4 domain-containing ion transport regulator 4 precursor (Channel
DE   inducing factor) (CHF).
GN   Name=FXD4;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=129/SvJ;
RT   "Genomic sequence of mouse CHF (FXD4)";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=C57BL/6J; TISSUE=Kidney;
RX   MEDLINE=223154683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaide I., Oeato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmeron S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedziński R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltchik L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Nunata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Waki J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki K., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573 (2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Kettner M., Madan A.C., Rodrigues S., Sanchez A.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
```

RA Farman N.;  
RT "Cellular localization and regulation of CHIF in kidney and colon.";  
RL Am. J. Physiol. 271:C793-C796(1996).  
CC -|- FUNCTION: Induces a potassium channel when expressed in Xenopus oocytes.  
CC -|- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -|- TISSUE SPECIFICITY: Selectively present in the distal parts of the nephron (medullary and papillary collecting ducts and end portions of cortical collecting tubule) and in the epithelial cells of the distal colon. No expression is found in renal proximal tubule, loop of henle and distal tubule, proximal colon, small intestine, lung, choroid plexus, salivary glands, or brain.  
CC -|- INDUCTION: By corticosteroids.  
CC -|- SIMILARITY: Belongs to the FXD family.  
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CC -----  
DR EMBL; L41254; AAA74691.1; -; mRNA.  
DR PIR; I59391; I59391.  
DR Ensembl; ENSRNOG00000014578; Rattus norvegicus.  
DR RGD; 70998; Fxyd4.  
DR GO; GO:0005267; F:potassium channel activity; IDA.  
DR InterPro; IPR000272; FXD.  
DR Pfam; PF02038; ATP1G1\_PLM\_MAT8; 1.  
DR PROSITE; PS01310; FXYD; 1.  
KW Ion transport; Ionic channel; Signal; Transmembrane; Transport.  
FT SIGNAL 1 20  
FT CHAIN 21 87  
FT TOPO DOM 21 38  
FT TRANSMEM 39 59  
FT TOPO DOM 60 87  
SQ SEQUENCE 87 AA; 9084 MW; 5D0DE1FPC6B1BCCA CRC64;  
Query Match 55.6%; Score 256.5; DB 1; Length 87;  
Best Local Similarity 61.5%; Pred. No. 1.9e-19;  
Matches 56; Conservative 11; Mismatches 17; Indels 7; Gaps 4;  
Qy 1 MERVTLA-LLLAGLTALEANDPANKDDPFYDWNKQLSGLICGGLLAAGIAAVLSG 59  
Db 1 MEGITCAFLVLAGLPVLEANGP-VDKGSPFYDWSLQGLGMIFGGLLCIAGIAMALSG 59  
Qy 60 KCKYKSKQKHSPP-VPEKALPLITPGSATT 88  
Db 60 KCK---CRRNHTPSSLPEKVTPLITPGSAST 87  
RESULT 6  
FXD3 MOUSE STANDARD; PRT; 88 AA.  
AC O61835;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE FXD domain-containing ion transport regulator 3 precursor (Chloride conductance inducer protein Mat-8) (Mammary tumor 8 kDa protein) (phospholemmann-like).  
DE Name=FXD3; Synonyms=Mat8, Plml;  
GN Mus musculus (Mouse).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=FVB/N; TISSUB=Mammary gland;  
RX MEDLINE=95060797; PubMed=7970700;  
RA Morrison B.W.; Leder P.;  
RT "neu and ras initiate murine mammary tumors that share genetic markers

generally absent in c-myc and int-2-initiated tumors.";  
OncoGene 9:3417-3426(1994).  
[2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUB=Mammary tumor;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.; Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.; Altshul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.; Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Haieh F.; Datchenko L.; Mariani K.; Farmer A.A.; Rubin G.M.; Hong L.; Scapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.; Brownstein M.J.; Ustin T.B.; Toshiyuki S.; Carninci P.; Prange C.; Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullany S.J.; Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.; Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.; Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.; Fahey J.; Helton E.; Kettman M.; Madan A.; Rodriguez S.; Sanchez A.; Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.; Blakeley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.; Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smailus D.E.; Schnerch A.; Schein J.E.; Jones S.J.M.; Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[3]  
RP EXPRESSION.  
RX MEDLINE=95138184; PubMed=7836447; DOI=10.1074/jbc.270.15.8571;  
RA Morrison B.W.; Moorman J.R.; Kowdley G.C.; Kobayashi Y.M.; Jones L.R.; Leder P.;  
RT "Mat-8, a novel phospholemmann-like protein expressed in human breast tumors, induces a chloride conductance in Xenopus oocytes."; J. Biol. Chem. 270:2176-2182(1995)  
CC -|- FUNCTION: Induces a hyperpolarization-activated chloride current when expressed in Xenopus oocytes. May be a modulator capable of activating endogenous oocyte channels.  
CC -|- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -|- TISSUE SPECIFICITY: Expressed in a subset of murine breast tumors.  
CC -|- MISCELLANEOUS: Marker of a cell type preferentially transformed by neu or ras oncoprotein.  
CC -|- SIMILARITY: Belongs to the FXYD family.  
CC -----  
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CC -----  
DR EMBL; X93038; CAA63606.1; -; mRNA.  
DR EMBL; BC002039; AAH02039.1; -; mRNA.  
DR EMBL; BC056223; AAH56223.1; -; mRNA.  
DR PIR; S61552; S61552.  
DR Ensembl; ENSMUSG000000057092; Mus musculus.  
DR MGI; MGI:107497; Fxyd3.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR InterPro; IPR000272; FXYD  
DR Pfam; PF02038; ATP1G1\_PLM\_MAT8; 1.  
DR PROSITE; PS01310; FXYD; 1.  
KW Chloride; Chloride channel; Ion transport; Ionic channel; Signal;  
KW Transmembrane; Transport.  
FT SIGNAL 1 20  
FT CHAIN 21 88  
FT TOPO DOM 21 38  
FT TRANSMEM 39 59  
FT TOPO DOM 60 88  
SQ SEQUENCE 88 AA; 9526 MW; 9CD61684B856E35D CRC64;  
Query Match 52.4%; Score 241.5; DB 1; Length 88;  
Best Local Similarity 57.8%; Pred. No. 7.5e-18;  
Matches 52; Conservative 11; Mismatches 24; Indels 3; Gaps 3;

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QY 1 MERVTLALL-LLAGLTALANDPANKDDPFYDWNKLNQLSLGCGLLAAGIAAVLSG 59
Db 1 MQEVLSLVVLGAGLPTUDNDP-ENKNDPPYDWSLVGGLICAGILCALGIIVLSG 59
QY 60 KCKYKSSQKHSPVPEKAIPITPGSATTC 89
Db 60 KCKCKFRQKP-SHRPGEGPLITPGSAHNC 88

RESULT 7
FXD3 RAT
ID FXD3 RAT STANDARD; PRT; 88 AA.
AC P59645;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE FXD domain-containing ion transport regulator 3 precursor.
GN Name=FXD3;
OS Rattus norvegicus (Rat);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lee N.H., Glodok A., Chandra I., Mason T.M., Quackenbush J.,
RA Kervilave A.R., Adams M.D.;
RA Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP RECONSTRUCTION FROM ESTS, AND CONCEPTUAL TRANSLATION.
RA MEDLINE=20408885; PubMed=10950925; DOI=10.1006/geno.2000.6274;
RA Sweadner K.J., Rael E.;
RT "The FXD gene family of small ion transport regulators or channels:
RT cDNA sequence, protein signature sequence, and expression.";
RL Genomics 68:41-56(2000).
CC -!- FUNCTION: Induces a hyperpolarization-activated chloride current
CC when expressed in Xenopus oocytes. May be a modulator capable of
CC activating endogenous oocyte channels.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the FXD family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AA01365; -; NOT ANNOTATED CDS; mRNA.
CC Ensembl; ENSRNOG0000021095; Rattus norvegicus.
CC InterPro; IPR000272; FXD.
CC Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
CC PROSITE; PS01310; FXD; 1.
CC KW Ion transport; Ionic channel; Signal; Transmembrane; Transport.
CC FT SIGNAL 1 20 Potential.
CC FT CHAIN 21 88 FXD domain-containing ion transport
CC FT regulator 3.
CC FT TOPO_DOM 21 38 Extracellular (Potential).
CC FT TRANSMEM 39 59 Potential.
CC FT TOPO_DOM 60 88 Cytoplasmic (Potential).
CC FT SEQUENCE 88 AA; 9411 MW; 45AF872FDIAF944 CRC64;
CC
CC Query Match 50.9%; Score 234.5; DB 1; Length 88;
CC Best Local Similarity 56.7%; Pred. No. 4.2e-17;
CC Matches 51; Conservative 10; Mismatches 26; Indels 3; Gaps 3;

QY 1 MERVTLALL-LLAGLTALANDPANKDDPFYDWNKLNQLSLGCGLLAAGIAAVLSG 59
Db 1 MQEVLSLVVLGAGLPTUDNDP-ENKNDPPYDWSLVGGLICAGILCALGIIVLSG 59
QY 60 KCKYKSSQKHSPVPEKAIPITPGSATTC 89
Db 60 KCKCKFRQKP-SHRPGDGPPLITPGSAHNC 88

RESULT 8
FXD3 FIG
ID FXD3 FIG STANDARD; PRT; 88 AA.
AC O97797;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE FXD domain-containing ion transport regulator 3 precursor (Chloride
DE conductance inducer protein Mat-8) (Mammary tumor 8 kDa protein).
GN Name=FXD3; Synonyms=MAT8;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OC NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Gastric mucosa;
RX MEDLINE=99140476; PubMed=10206733;
RA Maeda M., Hamano K., Hirano Y., Suzuki M., Takahashi E.-I., Terada T.,
RA Futai M., Sato R.;
RA "Structures of P-type transporting ATPases and chromosomal locations
RA of their genes.";
RT Cell Struct. Funct. 23:315-323(1998).
RL CC
CC -!- FUNCTION: Induces a hyperpolarization-activated chloride current
CC when expressed in Xenopus oocytes. May be a modulator capable of
CC activating endogenous oocyte channels.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the FXD family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AB015759; BAA35078.1; -; mRNA.
CC InterPro; IPR000272; FXD.
CC Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
CC PROSITE; PS01310; FXD; 1.
CC KW Chloride; Chloride channel; Ion transport; Ionic channel; Signal;
CC Transmembrane; Transport.
CC FT SIGNAL 1 17 Potential.
CC FT CHAIN 18 88 FXD domain-containing ion transport
CC FT regulator 3.
CC FT TOPO_DOM 18 38 Extracellular (Potential).
CC FT TRANSMEM 39 59 Potential.
CC FT TOPO_DOM 60 88 Cytoplasmic (Potential).
CC FT SEQUENCE 88 AA; 9314 MW; 6CC7810B90512E5A CRC64;
CC
CC Query Match 50.0%; Score 230.5; DB 1; Length 88;
CC Best Local Similarity 57.8%; Pred. No. 1.1e-16;
CC Matches 52; Conservative 10; Mismatches 25; Indels 3; Gaps 3;

QY 1 MERVTLA-LLLAGLTALANDPANKDDPFYDWNKLNQLSLGCGLLAAGIAAVLSG 59
Db 1 MHEVALSVLLIAGLSALDNDP-EDKNSPFYDWSLVGGLICAGITPCALGIIVLSG 59
QY 60 KCKYKSSQKHSPVPEKAIPITPGSATTC 89
Db 60 KCKCKFRQKP-SHRPGDGPPLITPGSAHNC 88

RESULT 9
FXD3 HUMAN
ID FXD3 HUMAN STANDARD; PRT; 87 AA.
AC Q14802; O13211;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE FXD domain-containing ion transport regulator 3 precursor (Chloride
```

conductance inducer protein Mat-8) (Mammary tumor 8 kDa protein) (Phospholemman-like).  
 DE Names=FXD3; Synonyms=MAT8, PLML;  
 DE Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RN TISSUE=Mammary gland;  
 RC MEDLINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.2426038999;  
 RC Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RC Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Stapleton M., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Brownstein M.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Bosak S.A., Wörley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Richardson S., Morley D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Villalón D.K., Wozny D., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buterfield Y.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: Induces a hyperpolarization-activated chloride current  
 when expressed in Xenopus oocytes. May be a modulator capable of  
 activating endogenous oocyte channels.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -!- TISSUE SPECIFICITY: Expressed in a subset of human breast tumors.  
 CC -!- MISCELLANEOUS: Marker of a cell type preferentially transformed by  
 neu or ras oncoprotein.  
 CC -!- SIMILARITY: Belongs to the FXD family.  
 CC -----  
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 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC -----  
 CC EMBL; X93036; CAA63604.1; -; mRNA.  
 CC EMBL; U28249; AAA73922.1; -; mRNA.  
 CC EMBL; BC005238; AAH05238.1; -; mRNA.  
 CC PIR; A55571; A55571.  
 CC Ensembl; ENSG00000089356; Homo sapiens.  
 CC HGNC; HGNC:4027; FXD3.  
 CC H-InvDB; HIX0018290; -.  
 CC MIM; 604996; -.  
 CC GO; GO:0003887; C:integral to plasma membrane; TAS.  
 CC GO; GO:0005254; F:chloride channel activity; TAS.  
 CC GO; GO:0006621; P:chloride transport; TAS.  
 CC InterPro; IPR000272; FXD.







OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 OC Canis.  
 OC NCBI\_TaxID=9615;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE (MRNA), AND PROTEIN SEQUENCE OF 21-92.  
 RC TISSUE=Heart ventricle;  
 RX MEDLINE=91250422; PubMed=1710217;  
 RA Palmer C.J., Scott B.T., Jones L.R.;  
 RT "Purification and complete sequence determination of the major plasma  
 RT membrane substrate for cAMP-dependent protein kinase and protein  
 RT kinase C in myocardium."  
 RL J. Biol. Chem. 266:11126-11130(1991).  
 CC -1- FUNCTION: Induces a hyperpolarization-activated chloride current  
 CC when expressed in Xenopus oocytes. May have a functional role in  
 CC muscle contraction.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Present in heart, esophagus, stomach, aorta,  
 CC skeletal muscle, smooth muscle, and liver but absent from brain  
 CC and kidney.  
 CC -1- PIM: Major plasma membrane substrate for cAMP-dependent protein  
 CC kinase (PK-A) and protein kinase C (PK-C) in several different  
 CC tissues. Phosphorylated in response to insulin and adrenergic  
 CC stimulation (By similarity).  
 CC -1- SIMILARITY: Belongs to the FXVD family.  
 CC -----  
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 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; M63934; -; NOT\_ANNOTATED\_CDS; mRNA.  
 CC PIR; A40533; A40533.  
 DR InterPro; IPR000272; FXVD.  
 DR Pfam; PF02038; ATP1G1\_PLM\_MAT8; 1.  
 DR PROSITE; PS01310; FXVD\_1.  
 KW Chloride; Chloride channel; Direct protein sequencing; Ion transport;  
 KW ionic channel; Phosphorylation; Signal; Transmembrane; Transport.  
 FT SIGNAL 1 20  
 FT CHAIN 21 92 Phospholemman.  
 FT TOPO\_DOM 21 35 Extracellular (Potential).  
 FT TRANSMEM 36 56 Potential.  
 FT TOPO\_DOM 57 92 Cytoplasmic (Potential).  
 FT MOD\_RES 83 83 Phosphoserine (by PKA and PKC) (By  
 FT similarity).  
 FT MOD\_RES 88 88 Phosphoserine (by PKA) (By similarity).  
 FT SEQUENCE 92 AA; 10500 MW; 890DE301BF8E740A CRC64;  
 Query Match 27.4%; Score 126.5; DB 1; Length 92;  
 Best Local Similarity 41.4%; Pred. No. 1.4e-05;  
 Matches 29; Conservative 15; Mismatches 23; Indels 3; Gaps 2;  
 QY 8 LLLAG-LTAAEANDPFANKDDPPYDWNKQLSLGICGGLAATAGIAAVLSGKYS 66  
 Db 8 LVLCVGLFATTATAP--QEHDPPTYDYSQSLRIGGLIAGILFILGILVLSRCRCXFN 65  
 QY 67 QKQHSVPPEK 76  
 Db 66 QQQRTGEPDE 75  
 RESULT 15  
 ID FXVD6 RAT STANDARD; PRT; 94 AA.  
 AC Q91XV6; Q9JLR4;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE FXVD domain-containing ion transport regulator 6 precursor (Vascular  
 DE endothelial cell specific protein 6) (VESP6) (phosphohippolin).  
 GN Name=Fxvd6; Synonyms=Php;  
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridea; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE (ISOFORM 1).  
 RC TISSUE=Liver;  
 RA Aoki T., Toyoda H., Nishimoto S., Tawara J., Komurasaki T.;  
 RT "Identification of VESP6, a vascular endothelial cell specific  
 RT protein.";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE (ISOFORM 2).  
 RC STRAIN=Sprague-Dawley; TISSUE=Hippocampus;  
 RX MEDLINE=21105932; PubMed=11165386; DOI=10.1016/S0169-328X(00)00213-8;  
 RA Yamaguchi F., Yamaguchi K., Tai Y., Sugimoto K., Tokuda M.;  
 RT "Molecular cloning and characterization of a novel phospholemmann-like  
 RT protein from rat hippocampus."  
 RL Brain Res. Mol. Brain Res. 86:189-192(2001).  
 RN [3]  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
 RC TISSUE=Lung;  
 RG NIH - Mammalian Gene Collection (MGC) project;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q91XV6-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q91XV6-2; Sequence=VSP\_001586;  
 CC -1- SIMILARITY: Belongs to the FXVD family.  
 CC -----  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; AB030908; BAB62242.1; -; mRNA.  
 CC EMBL; AF142439; AAF66613.1; -; mRNA.  
 CC EMBL; BC072528; AAH72528.1; -; mRNA.  
 CC Ensembl; ENSRNOG0000016412; Rattus norvegicus.  
 CC RGD; 69315; Fxyd6.  
 CC InterPro; IPR000272; FXVD  
 CC Pfam; PF02038; ATP1G1\_PLM\_MAT8; 1.  
 CC PROSITE; PS01310; FXVD; 1.  
 KW Alternative splicing; Ion transport; Ionic channel; Signal;  
 KW Transmembrane; Transport.  
 FT SIGNAL 1 17 Potential.  
 FT CHAIN 18 94 FXVD domain-containing ion transport  
 FT regulator 6.  
 FT TOPO\_DOM 18 34 Extracellular (Potential).  
 FT TRANSMEM 35 57 Potential.  
 FT TOPO\_DOM 58 94 Cytoplasmic (Potential).  
 FT VARSPLIC 20 20 Missing (in isoform 2).  
 FT CONFLICT 65 65 /FTId=VSP\_001586.  
 FT CONFLICT 65 65 N->S (in Ref. 2).  
 SQ SEQUENCE 94 AA; 10388 MW; 1C0D35FA0C572451 CRC64;  
 Query Match 27.0%; Score 124.5; DB 1; Length 94;  
 Best Local Similarity 37.5%; Pred. No. 2.4e-05;  
 Matches 33; Conservative 15; Mismatches 37; Indels 3; Gaps 2;  
 QY 1 MERYTALLLLAGLTAAEANDPFANKDDPPYDWNKQLSLGICGGLAATAGIAAVLSGK 60  
 Db 1 METVLLCSLLAPVVLASAAAEKEK-DPFYDYDTLRIGGLVFAVVLFSVGLILSR 59  
 QY 61 CKYKSSQKQHSVPPEKA--IPLITPGA 86  
 Db 60 CKCSFNQKPRAPGDDEAQAVENTITNAA 87



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Job time : 367 secs

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